GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:20 ; Search time 27.3926 Seconds
(without alignments)
195.980 Million cell updates/sec

Title: US-09-865-294A-51
Perfect score: 90
Sequence: 1 ISITEIKGVIVHRIETILF 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	90	100.0	19	6	AAE35657	Aae35657 Measles v
2	90	100.0	30	6	AAE35677	Aae35677 Human Abe
3	90	100.0	31	7	ADD89946	Add89946 CD4 pepti
4	90	100.0	32	6	AAE35678	Aae35678 Human Abe
5	90	100.0	34	6	AAE35679	Aae35679 Human Abe
6	90	100.0	45	7	ADD89951	Add89951 IgE pepti
7	90	100.0	48	6	AAE35680	Aae35680 Human Abe
8	90	100.0	50	7	ADD89944	Add89944 CD4 pepti
9	87	96.7	65	7	ADD89953	Add89953 Foot-and-
10	83	92.2	65	7	ADD89952	Add89952 Foot-and-
11	76	84.4	19	3	AAY68551	Aay68551 Helper T
12	76	84.4	19	3	AAY91135	Aay91135 Modified
13	76	84.4	19	5	ABG68202	Abg68202 Measles v
14	76	84.4	19	5	ABG68208	Abg68208 Measles v
15	76	84.4	19	6	AAE35653	Aae35653 Measles v
16	76	84.4	19	6	AAE35647	Aae35647 Measles v
17	76	84.4	19	6	AAE35644	Aae35644 Measles v
18	76	84.4	29	3	AAY91264	Aay91264 Modified
19	76	84.4	29	3	AAY91260	Aay91260 Modified
20	76	84.4	29	3	AAY91266	Aay91266 Modified
21	76	84.4	29	3	AAY91258	Aay91258 Modified
22	76	84.4	30	3	AAY91262	Aay91262 Modified
23	76	84.4	30	5	ABG68233	Abg68233 Optimised
24	76	84.4	31	3	AAY68582	Aay68582 Peptide i
25	76	84.4	31	3	AAY91173	Aay91173 Modified
26	76	84.4	31	3	AAY91268	Aay91268 Modified
27	76	84.4	32	5	ABG68235	Abg68235 Optimised
28	76	84.4	34	5	ABG68231	Abg68231 Optimised
29	76	84.4	34	6	AAE35681	Aae35681 Human Abe
30	76	84.4	35	3	AAY91242	Aay91242 Modified
31	76	84.4	36	3	AAY91224	Aay91224 Modified
32	76	84.4	36	3	AAY91234	Aay91234 Modified
33	76	84.4	36	3	AAY91238	Aay91238 Modified
34	76	84.4	39	5	ABG68237	Abg68237 Optimised
35	76	84.4	46	3	AAY91240	Aay91240 Modified
36	76	84.4	46	3	AAY91213	Aay91213 Modified
37	76	84.4	46	3	AAY91232	Aay91232 Modified
38	76	84.4	46	3	AAY80020	Aay80020 IgE immun
39	76	84.4	46	5	ABG68229	Abg68229 Optimised
40	76	84.4	46	5	ABG68227	Abg68227 Optimised
41	76	84.4	47	3	AAY68583	Aay68583 Peptide i
42	76	84.4	47	3	AAY91180	Aay91180 Inv epito
43	76	84.4	49	3	AAY91177	Aay91177 Modified
44	76	84.4	51	3	AAY91248	Aay91248 Modified
45	76	84.4	52	3	AAY91270	Aay91270 Modified

ALIGNMENTS

RESULT 1
AAE35657
ID AAE35657 standard; peptide; 19 AA.
XX
AC AAE35657;
XX
DT 17-JUN-2003 (first entry)
XX
DE Measles virus T helper cell epitope #31.
XX
KW Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic.
XX
OS Measles virus.
XX
PN WO200296350-A2.
XX
PD 05-DEC-2002.
XX
PF 02-APR-2002; 2002WO-US010293.
XX
PR 25-MAY-2001; 2001US-00865294.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2003-201258/19.
XX
PT Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.
XX
PS Claim 1; Page 37; 77pp; English.
XX
CC The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of

```
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is measles virus T helper (Th) cell epitope used in the
CC   exemplification of the invention
XX
SQ   Sequence 19 AA;

  Query Match             100.0%;  Score 90;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 2
AAE35677
ID   AAE35677 standard; peptide; 30 AA.
XX
AC   AAE35677;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #1.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .10
FT                   /note= "Human beta amyloid peptide"
FT   Region          14. .30
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Claim 9; Page 39; 77pp; English.
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 30 AA;

  Query Match             100.0%;  Score 90;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db         12 ISITEIKGVIVHRIETILF 30


RESULT 3
ADD89946
ID   ADD89946 standard; protein; 31 AA.
XX
AC   ADD89946;
XX
DT   29-JAN-2004  (first entry)
XX
DE   CD4 peptide used in immunostimulant complex for anti-HIV vaccine.
XX
KW   Immunostimulant; vaccine; human; immunogen; anti-HIV; immunotherapy; CD4.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   20
FT                   /note= "Epsilon-lysine"
XX
PN   WO2003068169-A2.
XX
PD   21-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004711.
XX
PR   14-FEB-2002; 2002US-00076674.
PR   31-JAN-2003; 2003US-00076674.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Sokoll KK;
XX
DR   WPI; 2003-778890/73.
XX
PT   Stabilized immunostimulating complex, useful for vaccination, e.g.
PT   against human immune deficiency viruses, comprises cationic peptide
PT   immunogen and anionic oligonucleotide.
XX
PS   Claim 14; SEQ ID NO 6; 159pp; English.
XX
CC   The present sequence is that of a synthetic immunogenic peptide derived
CC   from human CD4. This is an example of peptides that can be used in
CC   claimed immunostimulatory complexes of the invention that are
CC   specifically adapted to act as adjuvant and as peptide immunogen
CC   stabiliser. The complexes comprise a CpG oligonucleotide and a
CC   biologically active peptide immunogen. The complex is particulate and can
CC   efficiently present peptide immunogens to the cells of the immune system
CC   to produce an immune response. The complexes may be prepared with various
CC   ratios of peptides to CpG oligonucleotides to provide different physical
CC   properties, such as the size of the microparticle. An immunostimulatory
CC   complex comprising the present CD4 derived peptide can be used in an anti
CC   -CD4 immunotherapeutic vaccine for the treatment of HIV infection.
XX
SQ   Sequence 31 AA;
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  Query Match             100.0%;  Score 90;  DB 7;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 2e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 4
AAE35678
ID   AAE35678 standard; peptide; 32 AA.
XX
AC   AAE35678;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #2.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .12
FT                   /note= "Human beta amyloid peptide"
FT   Region          16. .32
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Claim 9; Page 39; 77pp; English.
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 32 AA;

  Query Match             100.0%;  Score 90;  DB 6;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db         14 ISITEIKGVIVHRIETILF 32


RESULT 5
AAE35679
ID   AAE35679 standard; peptide; 34 AA.
XX
AC   AAE35679;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #3.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .14
FT                   /note= "Human beta amyloid peptide"
FT   Region          18. .34
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Claim 9; Page 39; 77pp; English.
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
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CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 34 AA;

  Query Match             100.0%;  Score 90;  DB 6;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db         16 ISITEIKGVIVHRIETILF 34


RESULT 6
ADD89951
ID   ADD89951 standard; protein; 45 AA.
XX
AC   ADD89951;
XX
DT   29-JAN-2004  (first entry)
XX
DE   IgE peptide used in immunostimulant complex for allergy vaccine.
XX
KW   Immunostimulant; vaccine; human; immunogen; IgE; immunotherapy; allergy;
KW   antibody; antiallergic.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   20
FT                   /note= "Epsilon-lysine"
XX
PN   WO2003068169-A2.
XX
PD   21-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004711.
XX
PR   14-FEB-2002; 2002US-00076674.
PR   31-JAN-2003; 2003US-00076674.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Sokoll KK;
XX
DR   WPI; 2003-778890/73.
XX
PT   Stabilized immunostimulating complex, useful for vaccination, e.g.
PT   against human immune deficiency viruses, comprises cationic peptide
PT   immunogen and anionic oligonucleotide.
XX
PS   Claim 20; SEQ ID NO 11; 159pp; English.
XX
CC   The present sequence is that of a synthetic immunogenic peptide derived
CC   from human IgE. This is an example of peptides that can be used in
CC   claimed immunostimulatory complexes of the invention that are
CC   specifically adapted to act as adjuvant and as peptide immunogen
CC   stabiliser. The complexes comprise a CpG oligonucleotide and a
CC   biologically active peptide immunogen. The complex is particulate and can
CC   efficiently present peptide immunogens to the cells of the immune system
CC   to produce an immune response. The complexes may be prepared with various
CC   ratios of peptides to CpG oligonucleotides to provide different physical
CC   properties, such as the size of the microparticle. An immunostimulatory
CC   complex comprising the present IgE derived peptide can be used in an anti
CC   -IgE immunotherapeutic vaccine for the treatment of allergy.
XX
SQ   Sequence 45 AA;

  Query Match             100.0%;  Score 90;  DB 7;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 7
AAE35680
ID   AAE35680 standard; peptide; 48 AA.
XX
AC   AAE35680;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #4.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .28
FT                   /note= "Human beta amyloid peptide"
FT   Region          32. .48
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Claim 9; Page 39; 77pp; English.
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 48 AA;

  Query Match             100.0%;  Score 90;  DB 6;  Length 48;
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  Best Local Similarity   100.0%;  Pred. No. 3.5e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db         30 ISITEIKGVIVHRIETILF 48


RESULT 8
ADD89944
ID   ADD89944 standard; protein; 50 AA.
XX
AC   ADD89944;
XX
DT   29-JAN-2004  (first entry)
XX
DE   CD4  peptide used in immunostimulant complex as anti-HIV vaccine.
XX
KW   Immunostimulant; vaccine; human; immunogen; anti-HIV; immunotherapy.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   20
FT                   /note= "Epsilon-lysine"
XX
PN   WO2003068169-A2.
XX
PD   21-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004711.
XX
PR   14-FEB-2002; 2002US-00076674.
PR   31-JAN-2003; 2003US-00076674.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Sokoll KK;
XX
DR   WPI; 2003-778890/73.
XX
PT   Stabilized immunostimulating complex, useful for vaccination, e.g.
PT   against human immune deficiency viruses, comprises cationic peptide
PT   immunogen and anionic oligonucleotide.
XX
PS   Claim 14; SEQ ID NO 4; 159pp; English.
XX
CC   The present sequence is that of a synthetic immunogenic peptide derived
CC   from human CD4. This is an example of peptides that can be used in
CC   claimed immunostimulatory complexes of the invention that are
CC   specifically adapted to act as adjuvant and as peptide immunogen
CC   stabiliser. The complexes comprise a CpG oligonucleotide and a
CC   biologically active peptide immunogen. The complex is particulate and can
CC   efficiently present peptide immunogens to the cells of the immune system
CC   to produce an immune response. The complexes may be prepared with various
CC   ratios of peptides to CpG oligonucleotides to provide different physical
CC   properties, such as the size of the microparticle. An immunostimulatory
CC   complex comprising the present CD4 derived peptide can be used in an anti
CC   -CD4 immunotherapeutic vaccine for the treatment of HIV infection.
XX
SQ   Sequence 50 AA;

  Query Match             100.0%;  Score 90;  DB 7;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 9
ADD89953
ID   ADD89953 standard; protein; 65 AA.
XX
AC   ADD89953;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Foot-and-mouth disease peptide used in vaccine immunostimulant complex.
XX
KW   Immunostimulant; vaccine; immunogen; immunotherapy;
KW   foot-and-mouth disease.
XX
OS   Synthetic.
OS   Foot-and-mouth disease virus.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   20
FT                   /note= "Epsilon-lysine"
XX
PN   WO2003068169-A2.
XX
PD   21-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004711.
XX
PR   14-FEB-2002; 2002US-00076674.
PR   31-JAN-2003; 2003US-00076674.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Sokoll KK;
XX
DR   WPI; 2003-778890/73.
XX
PT   Stabilized immunostimulating complex, useful for vaccination, e.g.
PT   against human immune deficiency viruses, comprises cationic peptide
PT   immunogen and anionic oligonucleotide.
XX
PS   Claim 22; SEQ ID NO 13; 159pp; English.
XX
CC   The present sequence is that of a synthetic immunogenic peptide derived
CC   from foot-and-mouth disease (FMD) virus. This is an example of peptides
CC   that can be used in claimed immunostimulatory complexes of the invention
CC   that are specifically adapted to act as adjuvant and as peptide immunogen
CC   stabiliser. The complexes comprise a CpG oligonucleotide and a
CC   biologically active peptide immunogen. The complex is particulate and can
CC   efficiently present peptide immunogens to the cells of the immune system
CC   to produce an immune response. The complexes may be prepared with various
CC   ratios of peptides to CpG oligonucleotides to provide different physical
CC   properties, such as the size of the microparticle. An immunostimulatory
CC   complex comprising the present FMD virus derived peptide can be used in
CC   an anti-FMD vaccine for protective immunity against FMD.
XX
SQ   Sequence 65 AA;

  Query Match             96.7%;  Score 87;  DB 7;  Length 65;
  Best Local Similarity   94.7%;  Pred. No. 1.7e-07;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              ||||||||||||:||||||
Db          1 ISITEIKGVIVHKIETILF 19


RESULT 10
ADD89952
ID   ADD89952 standard; protein; 65 AA.
XX
AC   ADD89952;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Foot-and-mouth disease peptide used in vaccine immunostimulant complex.
```

XX
KW Immunostimulant; vaccine; immunogen; immunotherapy;
KW foot-and-mouth disease.
XX
OS Synthetic.
OS Foot-and-mouth disease virus.
XX
FH Key Location/Qualifiers
FT Modified-site 20
FT /note= "Epsilon-lysine"
XX
PN WO2003068169-A2.
XX
PD 21-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-US004711.
XX
PR 14-FEB-2002; 2002US-00076674.
PR 31-JAN-2003; 2003US-00076674.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Sokoll KK;
XX
DR WPI; 2003-778890/73.
XX
PT Stabilized immunostimulating complex, useful for vaccination, e.g.
PT against human immune deficiency viruses, comprises cationic peptide
PT immunogen and anionic oligonucleotide.
XX
PS Claim 22; SEQ ID NO 12; 159pp; English.
XX
CC The present sequence is that of a synthetic immunogenic peptide derived
CC from foot-and-mouth disease (FMD) virus. This is an example of peptides
CC that can be used in claimed immunostimulatory complexes of the invention
CC that are specifically adapted to act as adjuvant and as peptide immunogen
CC stabiliser. The complexes comprise a CpG oligonucleotide and a
CC biologically active peptide immunogen. The complex is particulate and can
CC efficiently present peptide immunogens to the cells of the immune system
CC to produce an immune response. The complexes may be prepared with various
CC ratios of peptides to CpG oligonucleotides to provide different physical
CC properties, such as the size of the microparticle. An immunostimulatory
CC complex comprising the present FMD virus derived peptide can be used in
CC an anti-FMD vaccine for protective immunity against FMD.
XX
SQ Sequence 65 AA;

Query Match 92.2%; Score 83; DB 7; Length 65;
Best Local Similarity 89.5%; Pred. No. 8.5e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISITEIKGVIVHRIETILF 19
||||:|||||||:||||||
Db 1 ISISEIKGVIVHKIETILF 19

RESULT 11
AAY68551
ID AAY68551 standard; peptide; 19 AA.
XX
AC AAY68551;
XX
DT 05-MAY-2000 (first entry)
XX
DE Helper T cell epitope derived from SSAL Th1.
XX
KW Structured synthetic antigen library; SSAL; helper T cell epitope;
KW SSAL1 Th1; F protein; Measles virus; peptide immunogen; LHRH;
KW luteinising hormone-releasing hormone; spermatogenesis; ovulation;
KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;
KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.
XX
OS Synthetic.
OS Measles virus.
XX
PN WO9966952-A1.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US013960.
XX
PR 20-JUN-1998; 98US-00100414.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160562/14.
XX
PT New peptide immunogen containing luteinizing hormone-releasing hormone
PT antigen site and helper T cell epitope, for e.g. contraception and
PT treatment of cancer.
XX
PS Claim 1; Page 29; 102pp; English.
XX
CC The present sequence represents a helper T cell epitope derived from a
CC structured synthetic antigen library (SSAL) helper T cell epitope
CC designated SSAL1 Th1. SSAL Th1 is modelled after a promiscuous epitope
CC taken from the F protein of the Measles virus. The present epitope is
CC designed to be used in tandem with a target antigen, luteinising hormone-
CC releasing hormone (LHRH). The epitope is used to construct peptide
CC immunogens of the invention, which contain at least one antigenic target
CC site, i.e. luteinising hormone-releasing hormone (LHRH) or its analogue,
CC and an artificial helper T cell epitope (Th). The peptide immunogens
CC cause induction of a specific immune response to LHRH which is involved
CC in regulation of spermatogenesis, ovulation, oestrus, sexual development
CC and secretion of sex hormones. Provision of a promiscuous T helper
CC epitope (which is functional in genetically diverse subjects) provides
CC optimum immunogenicity to the B cell epitopes of the target antigen and
CC thus high antibody titres against the target antigen. The peptide
CC immunogens of the invention are used to vaccinate against mammalian LHRH,
CC for use as (reversible) contraceptive; control of hormone-dependent
CC tumours (cancer of prostate or breast, also endometriosis); to prevent
CC boar taint (and improve meat quality) and for immunocastration
XX
SQ Sequence 19 AA;

Query Match 84.4%; Score 76; DB 3; Length 19;
Best Local Similarity 84.2%; Pred. No. 3e-06;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ISITEIKGVIVHRIETILF 19
|||:|||||||:|| |||
Db 1 ISISEIKGVIVHKIEGILF 19

RESULT 12
AAY91135
ID AAY91135 standard; peptide; 19 AA.
XX
AC AAY91135;
XX
DT 22-MAY-2000 (first entry)
XX
DE Modified measles virus F protein promiscuous Th epitope, SEQ ID NO:15.
XX
KW Promiscuous T-cell epitope; measles virus F protein; MVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KW cholesteryl ester transport protein; anti-arteriosclerotic.
XX
OS Measles virus.

OS Synthetic.
XX
PN WO9966957-A2.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US013975.
XX
PR 20-JUN-1998; 98US-00100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus.
XX
PS Claim 1; Page 54; 129pp; English.
XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and immunocastration)
CC ; for promoting the growth of animals; or for treating allergies or
CC arteriosclerosis. Incorporation of a promiscuous Th (functional in
CC genetically diverse subjects) into an immunogen improves capacity to
CC induce a strong T helper cell-mediated immune response, resulting in
CC production of antibodies against a target antigen. Th can replace carrier
CC proteins and pathogen-derived T helper epitopes. Sequence AAY91121
CC represents a promiscuous T helper epitope from the measles virus F (MVF)
CC protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246
CC represent synthetic Th epitopes based on the MVF Th epitope. Sequence
CC AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)
CC surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes
CC derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-
CC Y91244 are antigenic peptides comprising an LHRH sequence joined to a
CC promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide
CC used in these LHRH antigenic peptides. AAY91200 is somatostatin, and
CC AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th
CC epitope. Somatostatin immunogens may be used to promote growth in
CC livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and
CC AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may
CC be used to prevent HIV infection of T cells. AAY90212 is a modified
CC version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219
CC are Th epitope/IgE CH3 antigenic peptides which may be used in the
CC treatment of allergies. AAY91220 is a peptide derived from foot and mouth
CC disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this
CC peptide and a Th epitope. AAY91223 is a Plasmodium falciparum
CC circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS
CC antigen and an MVF Th epitope and may be used in a malaria vaccine.
CC AAY91228-Y91231 represent CETP-derived peptides and AAY91232-Y91241 are
CC immunogens comprising a CETP peptide and a Th epitope which may be used
CC to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247
CC and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-
CC Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and
CC HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1
CC vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory
CC invasin protein epitope from Yersinia species, and hinge spacer peptide,
CC both of which may optionally be used in the antigenic peptides of the
CC invention
XX
SQ Sequence 19 AA;

Query Match 84.4%; Score 76; DB 3; Length 19;
Best Local Similarity 84.2%; Pred. No. 3e-06;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ISITEIKGVIVHRIETILF 19
||||:|||||||:|| |||
Db 1 ISISEIKGVIVHKIEGILF 19

RESULT 13
ABG68202
ID ABG68202 standard; peptide; 19 AA.
XX
AC ABG68202;
XX
DT 07-OCT-2002 (first entry)
XX
DE Measles virus idealised helper T cell epitope #20.
XX
KW Immunogen; FimH adhesin functional site-derived target peptide; FAFSD;
KW helper T cell epitope; FimH; urinary tract infection;
KW type 1 fimbriated uropathogenic enterobacteria; vaccine;
KW FAFSD site-specific immunity; measles virus.
XX
OS Measles virus.
OS Synthetic.
XX
PN WO200251860-A2.
XX
PD 04-JUL-2002.
XX
PF 21-DEC-2001; 2001WO-US050816.
XX
PR 22-DEC-2000; 2000US-00747802.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2002-528681/56.
XX
PT Novel peptide immunogen, useful for evoking antibodies to prevent
PT adherence of Escherichia coli to bladder mucosa, comprises a FimH adhesin
PT functional site-derived target peptide covalently linked to helper T cell
PT epitope.
XX
PS Claim 18; Page 8; 62pp; English.
XX
CC The invention describes a peptide immunogen (I), comprising a helper T
CC cell epitope sequence (Th) or a carrier protein covalently attached to a
CC FimH adhesin functional site-derived (FAFSD) target peptide comprising
CC not more than 30 amino acids of the carbohydrate binding pocket of FimH,
CC or its crossreactive and immunologically functional analogue or mimetope.
CC (I) and a composition containing (I) are useful for inducing anti-FAFSD
CC peptide antibody production in a mammal. The composition is also useful
CC for reducing adherence to the urinary tract mucosa of a mammal by type 1
CC fimbriated uropathogenic enterobacteria (Escherichia coli) to prevent
CC urinary tract infection. (I) has a focused FAFSD site-specific immunity
CC together with a broad protective immunity, and with less adverse side
CC reactions than the more complex polypeptide subunit vaccines and the
CC carrier conjugated vaccine. Since (I) is chemically well defined it is
CC easy and less costly to manufacture and to control or assure the quality
CC of the product. This sequence represents a helper T cell epitope derived
CC from the measles virus used in the creation of a vaccine against urinary
CC tract infection
XX
SQ Sequence 19 AA;

Query Match 84.4%; Score 76; DB 5; Length 19;
Best Local Similarity 84.2%; Pred. No. 3e-06;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ISITEIKGVIVHRIETILF 19
              |||:|||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19
```

RESULT 14
ABG68208
ID ABG68208 standard; peptide; 19 AA.
XX
AC ABG68208;
XX
DT 07-OCT-2002 (first entry)
XX
DE Measles virus idealised helper T cell epitope #26.
XX
KW Immunogen; FimH adhesin functional site-derived target peptide; FAFSD;
KW helper T cell epitope; FimH; urinary tract infection;
KW type 1 fimbriated uropathogenic enterobacteria; vaccine;
KW FAFSD site-specific immunity; measles virus.
XX
OS Measles virus.
OS Synthetic.
XX
PN WO200251860-A2.
XX
PD 04-JUL-2002.
XX
PF 21-DEC-2001; 2001WO-US050816.
XX
PR 22-DEC-2000; 2000US-00747802.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2002-528681/56.
XX
PT Novel peptide immunogen, useful for evoking antibodies to prevent
PT adherence of Escherichia coli to bladder mucosa, comprises a FimH adhesin
PT functional site-derived target peptide covalently linked to helper T cell
PT epitope.
XX
PS Disclosure; Page 8; 62pp; English.
XX
CC The invention describes a peptide immunogen (I), comprising a helper T
CC cell epitope sequence (Th) or a carrier protein covalently attached to a
CC FimH adhesin functional site-derived (FAFSD) target peptide comprising
CC not more than 30 amino acids of the carbohydrate binding pocket of FimH,
CC or its crossreactive and immunologically functional analogue or mimetope.
CC (I) and a composition containing (I) are useful for inducing anti-FAFSD
CC peptide antibody production in a mammal. The composition is also useful
CC for reducing adherence to the urinary tract mucosa of a mammal by type 1
CC fimbriated uropathogenic enterobacteria (Escherichia coli) to prevent
CC urinary tract infection. (I) has a focused FAFSD site-specific immunity
CC together with a broad protective immunity, and with less adverse side
CC reactions than the more complex polypeptide subunit vaccines and the
CC carrier conjugated vaccine. Since (I) is chemically well defined it is
CC easy and less costly to manufacture and to control or assure the quality
CC of the product. This sequence represents a helper T cell epitope derived
CC from the measles virus used in the creation of a vaccine against urinary
CC tract infection
XX
SQ Sequence 19 AA;

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  Query Match             84.4%;  Score 76;  DB 5;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3e-06;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||:|||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19
```

RESULT 15
AAE35653
ID AAE35653 standard; peptide; 19 AA.
XX
AC AAE35653;
XX
DT 17-JUN-2003 (first entry)
XX
DE Measles virus T helper cell epitope #27.
XX
KW Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic.
XX
OS Measles virus.
XX
PN WO200296350-A2.
XX
PD 05-DEC-2002.
XX
PF 02-APR-2002; 2002WO-US010293.
XX
PR 25-MAY-2001; 2001US-00865294.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2003-201258/19.
XX
PT Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.
XX
PS Claim 1; Page 37; 77pp; English.
XX
CC The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is measles virus T helper (Th) cell epitope used in the
CC exemplification of the invention
XX
SQ Sequence 19 AA;

```
  Query Match             84.4%;  Score 76;  DB 6;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3e-06;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||:|||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


Search completed: June 18, 2004, 19:58:51
Job time : 28.3926 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:54:46 ; Search time 7.46012 Seconds
(without alignments)
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Perfect score: 90
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Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	76	84.4	19	3	US-09-100-414B-15	Sequence 15, Appl
2	76	84.4	19	3	US-09-303-323-15	Sequence 15, Appl
3	76	84.4	19	4	US-09-770-014-15	Sequence 15, Appl
4	76	84.4	31	3	US-09-100-414B-53	Sequence 53, Appl
5	76	84.4	31	3	US-09-303-323-53	Sequence 53, Appl
6	76	84.4	31	4	US-09-770-014-53	Sequence 53, Appl
7	76	84.4	35	3	US-09-100-414B-80	Sequence 80, Appl
8	76	84.4	35	3	US-09-303-323-80	Sequence 80, Appl
9	76	84.4	35	4	US-09-770-014-80	Sequence 80, Appl
10	76	84.4	46	3	US-09-100-414B-96	Sequence 96, Appl
11	76	84.4	46	3	US-09-303-323-96	Sequence 96, Appl
12	76	84.4	46	4	US-09-770-014-96	Sequence 96, Appl
13	76	84.4	47	3	US-09-100-414B-60	Sequence 60, Appl
14	76	84.4	47	3	US-09-303-323-60	Sequence 60, Appl
15	76	84.4	47	4	US-09-770-014-60	Sequence 60, Appl
16	76	84.4	49	3	US-09-100-414B-57	Sequence 57, Appl
17	76	84.4	49	3	US-09-303-323-57	Sequence 57, Appl
18	76	84.4	49	4	US-09-770-014-57	Sequence 57, Appl
19	76	84.4	80	3	US-09-100-600A-30	Sequence 30, Appl
20	71	78.9	19	3	US-09-100-414B-17	Sequence 17, Appl
21	71	78.9	19	3	US-09-303-323-17	Sequence 17, Appl
22	71	78.9	19	4	US-09-770-014-17	Sequence 17, Appl
23	71	78.9	31	3	US-09-100-414B-55	Sequence 55, Appl
24	71	78.9	31	3	US-09-303-323-55	Sequence 55, Appl
25	71	78.9	31	4	US-09-770-014-55	Sequence 55, Appl
26	69	76.7	19	3	US-09-100-414B-18	Sequence 18, Appl
27	69	76.7	19	3	US-09-100-414B-19	Sequence 19, Appl
28	69	76.7	19	3	US-09-100-414B-20	Sequence 20, Appl
29	69	76.7	19	3	US-09-303-323-18	Sequence 18, Appl
30	69	76.7	19	3	US-09-303-323-19	Sequence 19, Appl
31	69	76.7	19	3	US-09-303-323-20	Sequence 20, Appl
32	69	76.7	19	4	US-09-770-014-18	Sequence 18, Appl
33	69	76.7	19	4	US-09-770-014-19	Sequence 19, Appl
34	69	76.7	19	4	US-09-770-014-20	Sequence 20, Appl
35	69	76.7	31	3	US-09-100-414B-56	Sequence 56, Appl
36	69	76.7	31	3	US-09-100-414B-59	Sequence 59, Appl
37	69	76.7	31	3	US-09-100-414B-61	Sequence 61, Appl
38	69	76.7	31	3	US-09-303-323-56	Sequence 56, Appl
39	69	76.7	31	3	US-09-303-323-59	Sequence 59, Appl
40	69	76.7	31	3	US-09-303-323-61	Sequence 61, Appl
41	69	76.7	31	4	US-09-770-014-56	Sequence 56, Appl
42	69	76.7	31	4	US-09-770-014-59	Sequence 59, Appl
43	69	76.7	31	4	US-09-770-014-61	Sequence 61, Appl
44	69	76.7	35	3	US-09-100-414B-81	Sequence 81, Appl
45	69	76.7	35	3	US-09-303-323-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-09-100-414B-15
; Sequence 15, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-15

Query Match 84.4%; Score 76; DB 3; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.3e-07;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ISITEIKGVIVHRIETILF 19
              |||:||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19
```

RESULT 2

```
US-09-303-323-15
; Sequence 15, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/303,323
;      FILING DATE:  30-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-303-323-15

  Query Match             84.4%;  Score 76;  DB 3;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 4.3e-07;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||:|||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 3
US-09-770-014-15
; Sequence 15, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/770,014
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-15

  Query Match             84.4%;  Score 76;  DB 4;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 4.3e-07;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||:|||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 4
US-09-100-414B-53
; Sequence 53, Application US/09100414B
; Patent No. 6025468
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/100,414B
;      FILING DATE:  20-JUNE-1998
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-100-414B-53

  Query Match             84.4%;  Score 76;  DB 3;  Length 31;
  Best Local Similarity   84.2%;  Pred. No. 7.7e-07;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;
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```
Qy          1 ISITEIKGVIVHRIETILF 19
              |||:|||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 5
US-09-303-323-53
; Sequence 53, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/303,323
;      FILING DATE:  30-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-303-323-53

  Query Match             84.4%;  Score 76;  DB 3;  Length 31;
  Best Local Similarity   84.2%;  Pred. No. 7.7e-07;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||:|||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 6
US-09-770-014-53
; Sequence 53, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/770,014
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-53

  Query Match             84.4%;  Score 76;  DB 4;  Length 31;
  Best Local Similarity   84.2%;  Pred. No. 7.7e-07;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||:|||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 7
US-09-100-414B-80
; Sequence 80, Application US/09100414B
; Patent No. 6025468
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/100,414B
;      FILING DATE:  20-JUNE-1998
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  80:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-100-414B-80

  Query Match             84.4%;  Score 76;  DB 3;  Length 35;
  Best Local Similarity   84.2%;  Pred. No. 8.9e-07;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||:||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 8
US-09-303-323-80
; Sequence 80, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/303,323
;      FILING DATE:  30-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  80:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-303-323-80

  Query Match             84.4%;  Score 76;  DB 3;  Length 35;
  Best Local Similarity   84.2%;  Pred. No. 8.9e-07;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||:||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 9
US-09-770-014-80
; Sequence 80, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/770,014
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  80:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-80

  Query Match             84.4%;  Score 76;  DB 4;  Length 35;
  Best Local Similarity   84.2%;  Pred. No. 8.9e-07;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||:||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 10
US-09-100-414B-96
; Sequence 96, Application US/09100414B
; Patent No. 6025468
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/100,414B
;      FILING DATE:  20-JUNE-1998
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
```

```
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212-758-4800
;       TELEFAX:  212-751-6849
;   INFORMATION FOR SEQ ID NO:  96:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  46 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-09-100-414B-96

  Query Match             84.4%;  Score 76;  DB 3;  Length 46;
  Best Local Similarity   84.2%;  Pred. No. 1.2e-06;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||:||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 11
US-09-303-323-96
; Sequence 96, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/303,323
;      FILING DATE:  30-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  96:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  46 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-303-323-96

  Query Match             84.4%;  Score 76;  DB 3;  Length 46;
  Best Local Similarity   84.2%;  Pred. No. 1.2e-06;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||:||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 12
US-09-770-014-96
; Sequence 96, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/770,014
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  96:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  46 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-96

  Query Match             84.4%;  Score 76;  DB 4;  Length 46;
  Best Local Similarity   84.2%;  Pred. No. 1.2e-06;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||:||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 13
US-09-100-414B-60
; Sequence 60, Application US/09100414B
; Patent No. 6025468
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
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;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
;    LENGTH: 30
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-71

  Query Match           100.0%;  Score 90;  DB 10;  Length 30;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db         12 ISITEIKGVIVHRIETILF 30


RESULT 3
US-10-076-674-6
; Sequence 6, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/076,674
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;    LENGTH: 31
;    TYPE: PRT
;    ORGANISM: Human
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (20)..(20)
;    OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-6

  Query Match           100.0%;  Score 90;  DB 14;  Length 31;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 4
US-10-355-161A-6
; Sequence 6, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;    LENGTH: 31
;    TYPE: PRT
;    ORGANISM: Human
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (20)..(20)
;    OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-6

  Query Match           100.0%;  Score 90;  DB 15;  Length 31;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 5
US-09-865-294-72
; Sequence 72, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
;    LENGTH: 32
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-72

  Query Match           100.0%;  Score 90;  DB 10;  Length 32;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db         14 ISITEIKGVIVHRIETILF 32


RESULT 6
US-09-865-294-73
; Sequence 73, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
;    LENGTH: 34
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-73

  Query Match           100.0%;  Score 90;  DB 10;  Length 34;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db         16 ISITEIKGVIVHRIETILF 34


RESULT 7
US-10-076-674-11
; Sequence 11, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
```

```
;  CURRENT APPLICATION NUMBER: US/10/076,674
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 45
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-11

  Query Match             100.0%;  Score 90;  DB 14;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 8
US-10-355-161A-11
; Sequence 11, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 45
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-11

  Query Match             100.0%;  Score 90;  DB 15;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 9
US-09-865-294-74
; Sequence 74, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
;   LENGTH: 48
;   TYPE: PRT
;   ORGANISM: Measles virus
US-09-865-294-74

  Query Match             100.0%;  Score 90;  DB 10;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db         30 ISITEIKGVIVHRIETILF 48


RESULT 10
US-10-076-674-4
; Sequence 4, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/076,674
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 50
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-4

  Query Match             100.0%;  Score 90;  DB 14;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 3e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 11
US-10-355-161A-4
; Sequence 4, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 50
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-4

  Query Match             100.0%;  Score 90;  DB 15;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 3e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19
```

```
RESULT 12
US-10-355-161A-13
; Sequence 13, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
;   LENGTH: 65
;   TYPE: PRT
;   ORGANISM: Foot-and-mouth disease virus
US-10-355-161A-13

  Query Match             96.7%;  Score 87;  DB 15;  Length 65;
  Best Local Similarity   94.7%;  Pred. No. 1.4e-07;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              ||||||||||||:||||||
Db          1 ISITEIKGVIVHKIETILF 19


RESULT 13
US-10-355-161A-12
; Sequence 12, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 65
;   TYPE: PRT
;   ORGANISM: Foot-and-mouth disease virus
US-10-355-161A-12

  Query Match             92.2%;  Score 83;  DB 15;  Length 65;
  Best Local Similarity   89.5%;  Pred. No. 6.9e-07;
  Matches   17;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||:||||||||:||||||
Db          1 ISISEIKGVIVHKIETILF 19


RESULT 14
US-09-747-802-49
; Sequence 49, Application US/09747802
; Publication No. US20030027979A1
; GENERAL INFORMATION:
;  APPLICANT: WANG, CHANG YI
;  TITLE OF INVENTION: SYNTHETIC PEPTIDE COMPOSITION AS IMMUNOGENS FOR
;  TITLE OF INVENTION:  PREVENTION OF URINARY TRACT INFECTION
;  FILE REFERENCE: 1151-4165
;  CURRENT APPLICATION NUMBER: US/09/747,802
;  CURRENT FILING DATE:  2000-12-22
;  NUMBER OF SEQ ID NOS: 88
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  T HELPER
;   OTHER INFORMATION: SEQUENCE DERIVED FROM MEASLES VIRUS
US-09-747-802-49

  Query Match             84.4%;  Score 76;  DB 10;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.6e-06;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||:||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 15
US-09-747-802-55
; Sequence 55, Application US/09747802
; Publication No. US20030027979A1
; GENERAL INFORMATION:
;  APPLICANT: WANG, CHANG YI
;  TITLE OF INVENTION: SYNTHETIC PEPTIDE COMPOSITION AS IMMUNOGENS FOR
;  TITLE OF INVENTION:  PREVENTION OF URINARY TRACT INFECTION
;  FILE REFERENCE: 1151-4165
;  CURRENT APPLICATION NUMBER: US/09/747,802
;  CURRENT FILING DATE:  2000-12-22
;  NUMBER OF SEQ ID NOS: 88
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  T HELPER
;   OTHER INFORMATION: SEQUENCE DERIVED FROM MEASLES VIRUS
US-09-747-802-55

  Query Match             84.4%;  Score 76;  DB 10;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.6e-06;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ISITEIKGVIVHRIETILF 19
              |||:||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


Search completed: June 18, 2004, 20:23:46
Job time : 21.4479 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:45 ; Search time 5.71166 Seconds
(without alignments)
319.984 Million cell updates/sec

Title: US-09-865-294A-51
Perfect score: 90
Sequence: 1 ISITEIKGVIVHRIETILF 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	64	71.1	546	1	VGNZRL	cell fusion glycop
2	61	67.8	546	2	S47300	gene F protein - r
3	60	66.7	546	1	VGNZRK	cell fusion glycop
4	60	66.7	546	2	S55386	cell fusion protei
5	60	66.7	546	2	S47305	gene F protein - r
6	59	65.6	542	2	JQ2223	cell fusion protei
7	59	65.6	552	2	S47034	cell fusion protei
8	59	65.6	662	1	VGNZCD	cell fusion glycop
9	59	65.6	662	2	S21382	cell fusion protei
10	58	64.4	282	2	PQ0376	cell fusion glycop
11	58	64.4	282	2	PQ0388	cell fusion glycop
12	58	64.4	534	1	JU0274	cell fusion glycop
13	58	64.4	550	1	E48556	cell fusion glycop
14	58	64.4	553	1	VGNZMV	cell fusion glycop
15	58	64.4	631	1	VGNZPD	cell fusion glycop
16	58	64.4	631	1	A48346	cell fusion glycop
17	48	53.3	220	2	T00801	probable synaptobr
18	48	53.3	229	2	F86180	hypothetical prote
19	47	52.2	240	2	T47589	synaptobrevin-like
20	45	50.0	451	2	AH0063	conserved hypothet
21	45	50.0	636	2	S47299	gene F protein - r
22	44	48.9	175	2	D86180	hypothetical prote
23	44	48.9	221	2	F84741	probable synaptobr
24	43	47.8	708	2	T43109	cytolysin B transp
25	42.5	47.2	531	2	E82295	translation releas
26	42	46.7	236	2	A90190	hypothetical prote
27	42	46.7	329	2	T33378	hypothetical prote
28	42	46.7	1246	2	T00826	hypothetical prote
29	42	46.7	1816	2	A84845	probable ABC trans
30	41.5	46.1	428	2	A82215	probable alanine r
31	41	45.6	244	2	T43566	translocation lipo
32	41	45.6	244	2	A40049	virC-region lipopr
33	41	45.6	248	2	C83431	type III export pr
34	41	45.6	571	2	T38759	probable pyruvate
35	41	45.6	1140	2	S73786	hypothetical prote
36	41	45.6	2479	2	F87386	conserved hypothet
37	40	44.4	127	2	G69516	hypothetical prote
38	40	44.4	145	2	AI0110	hypothetical prote
39	40	44.4	166	2	T27540	hypothetical prote
40	40	44.4	263	2	H69336	cell division inhi
41	40	44.4	444	2	JC7084	alpha-1,3-mannosyl
42	40	44.4	456	2	B97129	probable metal-dep
43	40	44.4	457	2	T05651	hypothetical prote
44	40	44.4	565	1	VGNZSV	cell fusion glycop
45	40	44.4	565	1	VGNZSH	cell fusion glycop

ALIGNMENTS

RESULT 1
VGNZRL
cell fusion glycoprotein precursor - rinderpest virus (strain L)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: rinderpest virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Accession: A28921
R;Tsukiyama, K.; Yoshikawa, Y.; Yamanouchi, K.
Virology 164, 523-530, 1988
A;Title: Fusion glycoprotein (F) of rinderpest virus: entire nucleotide sequence of the
A;Reference number: A28921; MUID:88219541; PMID:3285575
A;Accession: A28921
A;Molecule type: mRNA
A;Residues: 1-546 <TSU>
A;Cross-references: GB:M20870; NID:g333898; PIDN:AAA47399.1; PID:g333899
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-104/Product: cell fusion glycoprotein F2 #status predicted <FG2>
F;105-546/Product: cell fusion glycoprotein F1 #status predicted <FG1>
F;109-133/Domain: transmembrane #status predicted <TN1>
F;485-513/Domain: transmembrane #status predicted <TN2>
F;25,57,63/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 71.1%; Score 64; DB 1; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.0087;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 SITEIKGVIVHRIETILF 19
              |::|||||||||:|:: :
Db        283 SLSEIKGVIVHRLESVSY 300
```

RESULT 2
S47300
gene F protein - rinderpest virus
C;Species: rinderpest virus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Oct-1999
C;Accession: S47300; PQ0865
R;Evans, S.A.; Baron, M.D.; Chamberlain, R.W.; Goatley, L.; Barrett, T.
submitted to the EMBL Data Library, March 1994
A;Description: The complete nucleotide sequence of the fusion protein gene of the vaccin
A;Reference number: S47299
A;Accession: S47300
A;Molecule type: DNA
A;Residues: 1-546 <EVA>
A;Cross-references: EMBL:Z31656; NID:g535406; PIDN:CAA83482.1; PID:g535407
R;Chamberlain, R.W.; Wamwayi, H.M.; Hockley, E.; Shaila, M.S.; Goatley, L.; Knowles, N.J
J. Gen. Virol. 74, 2775-2780, 1993
A;Title: Evidence for different lineages of rinderpest virus reflecting their geographic

```
A;Reference number: PQ0865; MUID:94103786; PMID:8277286
A;Accession: PQ0865
A;Molecule type: mRNA
A;Residues: 86-191 <CHA>
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein

  Query Match            67.8%;  Score 61;  DB 2;  Length 546;
  Best Local Similarity  61.1%;  Pred. No. 0.028;
  Matches   11;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              |::|||||||||:| : :
Db        283 SLSEIKGVIVHRLEGVSY 300


RESULT 3
VGNZRK
cell fusion glycoprotein precursor - rinderpest virus (strain Kabete O)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: rinderpest virus
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 25-Oct-1996
C;Accession: A31051
R;Hsu, D.; Yamanaka, M.; Miller, J.; Dale, B.; Grubman, M.; Yilma, T.
Virology 166, 149-153, 1988
A;Title: Cloning of the fusion gene of rinderpest virus: comparative sequence analysis w
A;Reference number: A31051; MUID:88322864; PMID:3413983
A;Accession: A31051
A;Molecule type: genomic RNA
A;Residues: 1-546 <HSU>
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-108/Product: cell fusion glycoprotein F2 #status predicted <FF1>
F;109-546/Product: cell fusion glycoprotein F1 #status predicted <FF2>
F;109-134/Domain: transmembrane #status predicted <TN1>
F;491-513/Domain: transmembrane #status predicted <TN2>
F;25,57,63,518/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            66.7%;  Score 60;  DB 1;  Length 546;
  Best Local Similarity  55.6%;  Pred. No. 0.041;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              |::|||||:||:| : :
Db        283 SLSEIKGVIIHRLEGVSY 300


RESULT 4
S55386
cell fusion protein - peste-des-petits-ruminants virus (strain 75/1)
N;Alternate names: F protein
C;Species: peste-des-petits-ruminants virus
A;Variety: strain 75/1
C;Date: 23-May-1997 #sequence_revision 23-May-1997 #text_change 20-Sep-1999
C;Accession: S55386
R;Meyer, G.; Diallo, A.
submitted to the EMBL Data Library, September 1994
A;Description: The nucleotide sequence of fusion protein gene of the Peste des petits ru
to each virus.
A;Reference number: S55386
A;Accession: S55386
A;Molecule type: DNA
A;Residues: 1-546 <MEY>
A;Cross-references: EMBL:Z37017; NID:g854372; PIDN:CAA85451.1; PID:g854373
A;Experimental source: strain 75/1; cell line vero
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: membrane fusion

  Query Match            66.7%;  Score 60;  DB 2;  Length 546;
  Best Local Similarity  61.1%;  Pred. No. 0.041;
  Matches   11;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|||||||||:|| | :
Db        283 TLSEIKGVIVHKIEAISY 300


RESULT 5
S47305
gene F protein - rinderpest virus
C;Species: rinderpest virus
C;Date: 20-Oct-1994 #sequence_revision 08-Sep-1995 #text_change 20-Sep-1999
C;Accession: S47305; S47301
R;Baron, M.D.; Barrett, T.
submitted to the EMBL Data Library, March 1994
A;Description: The sequence of the N and L genes of Rinderpest virus, and the 5O and 3O
A;Reference number: S47283
A;Accession: S47305
A;Molecule type: mRNA
A;Residues: 1-546 <BAR>
A;Cross-references: EMBL:Z30697; NID:g535396; PIDN:CAA83181.1; PID:g535401; EMBL:Z30700
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: transmembrane protein

  Query Match            66.7%;  Score 60;  DB 2;  Length 546;
  Best Local Similarity  55.6%;  Pred. No. 0.041;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              |::|||||:||:| : :
Db        283 SLSEIKGVIIHRLEGVSY 300


RESULT 6
JQ2223
cell fusion protein F0 precursor - phocine distemper virus
N;Contains: F1 and F2 chains
C;Species: phocine distemper virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 24-Nov-1999
C;Accession: JQ2223
R;Visser, I.K.G.; van der Heijden, R.W.J.; van de Bildt, M.W.G.; Kenter, M.J.H.; Oervel
J. Gen. Virol. 74, 1989-1994, 1993
A;Title: Fusion protein gene nucleotide sequence similarities, shared antigenic sites a
e virus entity.
A;Reference number: JQ2223; MUID:93389459; PMID:8376973
A;Accession: JQ2223
A;Molecule type: mRNA
A;Residues: 1-542 <VIS>
A;Cross-references: GB:L07075
A;Note: the authors translated the codon ATC for residue 4 as Leu
C;Comment: This fusion protein F0 is cleaved into F1 and F2 chains.
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-542/Product: fusion protein #status predicted <MAT>
F;16-99/Product: F2 chain #status predicted <F2C>
F;105-542/Product: F1 chain #status predicted <F1C>
F;105-135/Region: hydrophobic
F;486-512/Domain: transmembrane #status predicted <TMM>
F;21,53,59,397/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            65.6%;  Score 59;  DB 2;  Length 542;
  Best Local Similarity  50.0%;  Pred. No. 0.06;
  Matches    9;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|:|||||||:| : :
```

```
Db        279 TLSEVKGVIVHRLEAVSY 296


RESULT 7
S47034
cell fusion protein precursor - porpoise morbillivirus
N;Alternate names: F protein
C;Species: porpoise morbillivirus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C;Accession: S47034
R;Bolt, G.; Gottschalck, E.; Blixenkkrone-Moeller, M.; Wishaupt, R.G.A.; Welsh, M.J.; Ea
submitted to the EMBL Data Library, July 1994
A;Description: Nucleotide sequence comparisons of the F and M genes of cetacean morbilli
A;Reference number: S47034
A;Accession: S47034
A;Molecule type: mRNA
A;Residues: 1-552 <BOL>
A;Cross-references: EMBL:X80757; NID:g520639; PIDN:CAA56731.1; PID:g520640
A;Experimental source: isolate Ulster 88
A;Note: the source is designated as Cetacean morbillivirus
C;Superfamily: parainfluenza virus cell fusion protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-552/Product: fusion protein #status predicted <MAT>

  Query Match             65.6%;  Score 59;  DB 2;  Length 552;
  Best Local Similarity   50.0%;  Pred. No. 0.061;
  Matches    9;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|:|||||||:| : :
Db        289 TLSEVKGVIVHRLEAVSY 306


RESULT 8
VGNZCD
cell fusion glycoprotein precursor - canine distemper virus
N;Contains: fusion protein F1; fusion protein F2
C;Species: canine distemper virus
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C;Accession: JS0321
R;Barrett, T.; Clarke, D.K.; Evans, S.A.; Rima, B.K.
Virus Res. 8, 373-386, 1987
A;Title: The nucleotide sequence of the gene encoding the F protein of canine distemper
A;Reference number: JS0321; MUID:88129050; PMID:3433924
A;Accession: JS0321
A;Molecule type: mRNA
A;Residues: 1-662 <BAR>
A;Cross-references: GB:M21849; NID:g323241; PIDN:AAA42878.1; PID:g323242
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-135/Domain: signal sequence #status predicted <SIG>
F;136-224/Product: cell fusion glycoprotein F2 #status predicted <F2P>
F;225-662/Product: cell fusion glycoprotein F1 #status predicted <F1P>
F;606-629/Domain: transmembrane #status predicted <MEM>
F;62,141,173,179,517/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             65.6%;  Score 59;  DB 1;  Length 662;
  Best Local Similarity   50.0%;  Pred. No. 0.074;
  Matches    9;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|:|||||||:| : :
Db        399 TLSEVKGVIVHRLEAVSY 416


RESULT 9
S21382
cell fusion protein - canine distemper virus
C;Species: canine distemper virus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C;Accession: S21382
R;Wild, T.F.; Bernard, A.; Spehner, D.; Villeval, D.; Drillien, R.
submitted to the EMBL Data Library, April 1992
A;Description: Vaccination of mice against canine distemper virus induced encephalitis v
A;Reference number: S21382
A;Accession: S21382
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-662 <WIL>
A;Cross-references: EMBL:X65509; NID:g58853; PIDN:CAA46481.1; PID:g58854
C;Superfamily: parainfluenza virus cell fusion protein

  Query Match             65.6%;  Score 59;  DB 2;  Length 662;
  Best Local Similarity   50.0%;  Pred. No. 0.074;
  Matches    9;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|:|||||||:| : :
Db        399 TLSEVKGVIVHRLEAVSY 416


RESULT 10
PQ0376
cell fusion glycoprotein - measles virus (strain TT) (fragment)
C;Species: measles virus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Nov-1999
C;Accession: PQ0376
R;Schulz, T.F.; Hoad, J.G.; Whitby, D.; Tizard, E.J.; Dillon, M.J.; Weiss, R.A.
J. Gen. Virol. 73, 1581-1586, 1992
A;Title: A measles virus isolate from a child with Kawasaki disease: sequence comparisor
A;Reference number: PQ0374; MUID:92300360; PMID:1607874
A;Accession: PQ0376
A;Molecule type: genomic RNA
A;Residues: 1-282 <SCH>
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion

  Query Match             64.4%;  Score 58;  DB 2;  Length 282;
  Best Local Similarity   55.6%;  Pred. No. 0.046;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::||||||||:| : :
Db         19 TLSEIKGVIVHRLEGVSY 36


RESULT 11
PQ0388
cell fusion glycoprotein - measles virus (strain Schwarz vaccine) (fragment)
C;Species: measles virus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Nov-1999
C;Accession: PQ0388
R;Schulz, T.F.; Hoad, J.G.; Whitby, D.; Tizard, E.J.; Dillon, M.J.; Weiss, R.A.
J. Gen. Virol. 73, 1581-1586, 1992
A;Title: A measles virus isolate from a child with Kawasaki disease: sequence comparisor
A;Reference number: PQ0374; MUID:92300360; PMID:1607874
A;Accession: PQ0388
A;Molecule type: genomic RNA
A;Residues: 1-282 <SCH>
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion

  Query Match             64.4%;  Score 58;  DB 2;  Length 282;
  Best Local Similarity   55.6%;  Pred. No. 0.046;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::||||||||:| : :
Db         19 TLSEIKGVIVHRLEGVSY 36
```

```
RESULT 12
JU0274
cell fusion glycoprotein precursor - subacute sclerosing panencephalitis virus (strain Y
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: subacute sclerosing panencephalitis virus, SSPEV
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000
C;Accession: JU0274
R;Komase, K.; Haga, T.; Yoshikawa, Y.; Sato, T.A.; Yamanouchi, K.
Virus Genes 4, 173-181, 1990
A;Title: Molecular analysis of structural protein genes of the Yamagata-1 strain of defe
A;Reference number: JU0274; MUID:90385702; PMID:1698327
A;Accession: JU0274
A;Molecule type: mRNA
A;Residues: 1-534 <KOM>
A;Cross-references: EMBL:D10548; NID:g222256; PIDN:BAA01405.1; PID:g222257
A;Note: the authors translated the codon GTA for residue 459 as Gly and GGG for residue
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-107/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F;108-534/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F;498-514/Domain: transmembrane #status predicted <TMN>
F;6,29,61,67/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             64.4%;  Score 58;  DB 1;  Length 534;
  Best Local Similarity   55.6%;  Pred. No. 0.088;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|||||||||:| : :
Db        287 TLSEIKGVIVHRLEGVSY 304


RESULT 13
E48556
cell fusion glycoprotein precursor - measles virus (strain AIK-C)
C;Species: measles virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C;Accession: E48556
R;Mori, T.; Sasaki, K.; Hashimoto, H.; Makino, S.
Virus Genes 7, 67-81, 1993
A;Title: Molecular cloning and complete nucleotide sequence of genomic RNA of the AIK-C
A;Reference number: A48556; MUID:93227570; PMID:8470368
A;Accession: E48556
A;Molecule type: genomic RNA
A;Residues: 1-550 <MOR>
A;Cross-references: GB:S58435; NID:g299460; PIDN:AAB26145.1; PID:g299465
A;Note: sequence extracted from NCBI backbone (NCBIN:129264, NCBIP:129272)
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-107/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F;108-550/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F;113-138/Region: hydrophobic
F;495-514/Domain: transmembrane #status predicted <TMM>
F;6,29,61,67/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             64.4%;  Score 58;  DB 1;  Length 550;
  Best Local Similarity   55.6%;  Pred. No. 0.09;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|||||||||:| : :
Db        287 TLSEIKGVIVHRLEGVSY 304


RESULT 14
VGNZMV
cell fusion glycoprotein precursor - measles virus
C;Species: measles virus
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1989 #text_change 16-Jun-2000
C;Accession: A26962; A25616; PQ0380; PQ0384
R;Buckland, R.; Gerald, C.; Barker, R.; Wild, T.F.
J. Gen. Virol. 68, 1695-1703, 1987
A;Title: Fusion glycoprotein of measles virus: nucleotide sequence of the gene and comp
A;Reference number: A92794; MUID:87224816; PMID:3585281
A;Accession: A26962
A;Molecule type: mRNA
A;Residues: 1-553 <BUC>
A;Cross-references: GB:D00090; NID:g222061; PIDN:BAA00056.1; PID:g222062
A;Experimental source: strain Halle
R;Richardson, C.; Hull, D.; Greer, P.; Hasel, K.; Berkovich, A.; Englund, G.; Bellini,
Virology 155, 508-523, 1986
A;Title: The nucleotide sequence of the mRNA encoding the fusion protein of measles vir
A;Reference number: A94350; MUID:87071668; PMID:3788062
A;Accession: A25616
A;Molecule type: mRNA
A;Residues: 4-553 <RIC>
A;Cross-references: GB:M14915; NID:g331762; PIDN:AAA46423.1; PID:g331763
A;Experimental source: strain Edmonston
R;Schulz, T.F.; Hoad, J.G.; Whitby, D.; Tizard, B.J.; Dillon, M.J.; Weiss, R.A.
J. Gen. Virol. 73, 1581-1586, 1992
A;Title: A measles virus isolate from a child with Kawasaki disease: sequence comparisc
A;Reference number: PQ0374; MUID:92300360; PMID:1607874
A;Accession: PQ0380
A;Molecule type: genomic RNA
A;Residues: 272-553 <SCH1>
A;Experimental source: isolate CL
A;Accession: PQ0384
A;Molecule type: genomic RNA
A;Residues: 272-553 <SCH2>
A;Experimental source: isolate SE
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-110/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F;111-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F;501-517/Domain: transmembrane #status predicted <TMN>
F;32,64,70/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             64.4%;  Score 58;  DB 1;  Length 553;
  Best Local Similarity   55.6%;  Pred. No. 0.091;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|||||||||:| : :
Db        290 TLSEIKGVIVHRLEGVSY 307


RESULT 15
VGNZPD
cell fusion glycoprotein precursor - phocine distemper virus
N;Contains: fusion protein F1; fusion protein F2
C;Species: phocine distemper virus
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 25-Oct-1996
C;Accession: JQ1368
R;Koevamees, J.; Blixenkrone-Moeller, M.; Sharma, B.; Oervell, C.; Norrby, E.
J. Gen. Virol. 72, 2959-2966, 1991
A;Title: The nucleotide sequence and deduced amino acid composition of the haemagglutin
A;Reference number: JQ1368; MUID:92113538; PMID:1765768
A;Accession: JQ1368
A;Molecule type: genomic RNA
A;Residues: 1-631 <KOV>
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-188/Product: cell fusion glycoprotein F2 #status predicted <FP2>
F;89-106/Domain: transmembrane #status predicted <TM1>
```

F;189-193/Region: cleavage processing #status predicted
F;194-631/Product: cell fusion glycoprotein F1 #status predicted <FP1>
F;194-212/Domain: transmembrane #status predicted <TM2>
F;575-595/Domain: transmembrane #status predicted <TM3>
F;110,142,148,486/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.4%; Score 58; DB 1; Length 631;
Best Local Similarity 44.4%; Pred. No. 0.1;
Matches 8; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 SITEIKGVIVHRIETILF 19
              :::|:|||:|||:| : :
Db        368 TLSEVKGVVVHRLEAVSY 385
```

Search completed: June 18, 2004, 20:03:29
Job time : 6.71166 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:55 ; Search time 3.73006 Seconds
(without alignments)
265.232 Million cell updates/sec

Title: US-09-865-294A-51
Perfect score: 90
Sequence: 1 ISITEIKGVIVHRIETILF 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	64	71.1	546	1	VGLF_RINDL	P10864 rinderpest
2	61	67.8	546	1	VGLF_RINDB	P41360 rinderpest
3	60	66.7	546	1	VGLF_RINDR	P41356 rinderpest
4	59	65.6	662	1	VGLF_CDVO	P12569 canine dist
5	58	64.4	534	1	VGLF_MBASY	P26032 measles vir
6	58	64.4	550	1	VGLF_MEASA	P35973 measles vir
7	58	64.4	550	1	VGLF_MBASE	P08300 measles vir
8	58	64.4	631	1	VGLF_PHODV	P28886 phocine dis
9	54	60.0	546	1	VGLF_RINDK	P12574 rinderpest
10	50	55.6	529	1	VGLF_MBASI	P26031 measles vir
11	48	53.3	220	1	V725_ARATH	O48850 arabidopsis
12	48	53.3	229	1	V726_ARATH	Q9mas5 arabidopsis
13	47	52.2	240	1	V727_ARATH	Q9m376 arabidopsis
14	44	48.9	219	1	V721_ARATH	Q9ztw3 arabidopsis
15	44	48.9	221	1	V722_ARATH	P47192 arabidopsis
16	42.5	47.2	529	1	RF3_VIBPA	Q87m18 vibrio para
17	42.5	47.2	529	1	RF3_VIBVU	Q8dbt6 vibrio vuln
18	42.5	47.2	529	1	RF3_VIBVY	Q7mi34 vibrio vuln
19	42.5	47.2	531	1	RF3_VIBCH	Q9ku64 vibrio chol
20	41.5	46.1	392	1	ALR2_VIBCH	Q9kse5 vibrio chol
21	41	45.6	244	1	YSCJ_YEREN	Q01251 yersinia en
22	41	45.6	244	1	YSCJ_YERPE	Q00926 yersinia pe
23	41	45.6	571	1	DCP1_SCHPO	Q09737 schizosacch
24	41	45.6	1140	1	YD76_MYCPN	P75405 mycoplasma
25	40	44.4	127	1	YL35_ARCFU	O28145 archaeoglob
26	40	44.4	208	1	PSD_METMA	Q8px20 methanosarc
27	40	44.4	235	1	PUR7_THETN	Q8rc58 thermoanaer
28	40	44.4	565	1	VGLF_SENDF	P12575 sendai viru
29	40	44.4	565	1	VGLF_SENDH	P04856 sendai viru
30	40	44.4	565	1	VGLF_SENDJ	P04854 sendai viru
31	40	44.4	565	1	VGLF_SENDZ	P04855 sendai viru
32	39	43.3	145	1	FABZ_RICPR	Q9zed4 rickettsia
33	39	43.3	204	1	GIDB_COXBU	P94614 coxiella bu
34	39	43.3	274	1	VGLE_HSV2	P13289 herpes simp
35	39	43.3	338	1	SYFA_FUSNN	Q8rhb4 fusobacteri
36	39	43.3	365	1	GRAB_BACSU	P07869 bacillus su
37	39	43.3	381	1	ARGE_BUCAI	P57155 buchnera ap
38	39	43.3	397	1	MPA2_AMBAR	P27762 ambrosia ar
39	39	43.3	701	1	TP20_YEAST	P33891 saccharomyc
40	39	43.3	891	1	SECA_PAVLU	Q01570 pavlova lut
41	39	43.3	915	1	SYA_METKA	Q8twy1 methanopyru
42	39	43.3	1704	1	VIT1_FUNHE	Q90508 fundulus he
43	38	42.2	141	1	FAZ2_ENTFA	Q820t5 enterococcu
44	38	42.2	198	1	PGD2_CHICK	O73888 gallus gall
45	38	42.2	208	1	PSD_METAC	Q8tuf2 methanosarc

ALIGNMENTS

RESULT 1
VGLF_RINDL
ID VGLF_RINDL STANDARD; PRT; 546 AA.
AC P10864;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Rinderpest virus (strain L) (RDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11243;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219541; PubMed=3285575;
RA Tsukiyama K., Yoshikawa Y., Yamanouchi K.;
RT "Fusion glycoprotein (F) of rinderpest virus: entire nucleotide
RT sequence of the F mRNA, and several features of the F protein.";
RL Virology 164:523-530(1988).
CC -!- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC ---

CC ---
DR EMBL; M20870; AAA47399.1; -.
DR PIR; A28921; VGNZRL.
DR HSSP; P04849; 1SVF.
DR InterPro; IPR000776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 546 FUSION GLYCOPROTEIN F0.
FT CHAIN 20 108 F2 PROTEIN.
FT CHAIN 109 546 F1 PROTEIN.
FT DOMAIN 104 108 ARG/LYS-RICH (BASIC).
FT TRANSMEM 109 133 POTENTIAL.
FT TRANSMEM 484 513 POTENTIAL.
FT DOMAIN 514 517 ARG/LYS-RICH (BASIC).
FT DISULFID 64 191 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 546 AA; 58911 MW; 985029418F28FFB5 CRC64;

```
  Query Match             71.1%;  Score 64;  DB 1;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 0.0028;
  Matches   11;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              |::|||||||||:|:: :
Db        283 SLSEIKGVIVHRLESVSY 300


RESULT 2
VGLF_RINDB
ID   VGLF_RINDB     STANDARD;      PRT;   546 AA.
AC   P41360;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Rinderpest virus (strain RBT1) (RDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=39007;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95088609; PubMed=7996154;
RA   Evans S.A., Baron M.D., Chamberlain R.W., Goatley L., Barrett T.;
RT   "Nucleotide sequence comparisons of the fusion protein gene from
RT   virulent and attenuated strains of rinderpest virus.";
RL   J. Gen. Virol. 75:3611-3617(1994).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z31656; CAA83482.1; -.
DR   PIR; S47300; S47300.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    546       FUSION GLYCOPROTEIN F0.
FT   CHAIN        20    108       F2 PROTEIN.
FT   CHAIN       109    546       F1 PROTEIN.
FT   DOMAIN      104    108       ARG/LYS-RICH (BASIC).
FT   TRANSMEM    109    133       POTENTIAL.
FT   TRANSMEM    484    513       POTENTIAL.
FT   DOMAIN      514    517       ARG/LYS-RICH (BASIC).
FT   DISULFID     64    191       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD     25     25       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     57     57       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     63     63       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    518    518       O-LINKED (POTENTIAL).
SQ   SEQUENCE   546 AA;  58418 MW;  38B539B89344F401 CRC64;

  Query Match             67.8%;  Score 61;  DB 1;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 0.0093;
  Matches   11;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              |::|||||||||:| : :
Db        283 SLSEIKGVIVHRLEGVSY 300


RESULT 3
VGLF_RINDR
ID   VGLF_RINDR     STANDARD;      PRT;   546 AA.
AC   P41356;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Rinderpest virus (strain RBOK) (RDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=36409;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95088609; PubMed=7996154;
RA   Evans S.A., Baron M.D., Chamberlain R.W., Goatley L., Barrett T.;
RT   "Nucleotide sequence comparisons of the fusion protein gene from
RT   virulent and attenuated strains of rinderpest virus.";
RL   J. Gen. Virol. 75:3611-3617(1994).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z30700; CAA83186.1; -.
DR   EMBL; Z30697; CAA83181.1; -.
DR   PIR; S47305; S47305.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    546       FUSION GLYCOPROTEIN F0.
FT   CHAIN        20    108       F2 PROTEIN.
FT   CHAIN       109    546       F1 PROTEIN.
FT   DOMAIN      104    108       ARG/LYS-RICH (BASIC).
FT   TRANSMEM    109    133       POTENTIAL.
FT   TRANSMEM    484    513       POTENTIAL.
FT   DOMAIN      514    517       ARG/LYS-RICH (BASIC).
FT   DISULFID     64    191       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD     25     25       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     57     57       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     63     63       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    518    518       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   546 AA;  58705 MW;  ED3DF8AFFDBECB95 CRC64;

  Query Match             66.7%;  Score 60;  DB 1;  Length 546;
  Best Local Similarity   55.6%;  Pred. No. 0.014;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              |::||||||:||:| : :
Db        283 SLSEIKGVIIHRLEGVSY 300


RESULT 4
VGLF_CDVO
ID   VGLF_CDVO      STANDARD;      PRT;   662 AA.
AC   P12569; Q65991;
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DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Canine distemper virus (strain Onderstepoort) (CDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11233;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88129050; PubMed=3433924;
RA   Barrett T., Clarke D.K., Evans S.A., Rima B.K.;
RT   "The nucleotide sequence of the gene encoding the P protein of canine
RT   distemper virus: a comparison of the deduced amino acid sequence with
RT   other paramyxoviruses.";
RL   Virus Res. 8:373-386(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93227696; PubMed=8470428;
RA   Wild T.F., Bernard A., Spehner D., Villeval D., Drillien R.;
RT   "Vaccination of mice against canine distemper virus-induced
RT   encephalitis with vaccinia virus recombinants encoding measles or
RT   canine distemper virus antigens.";
RL   Vaccine 11:438-444(1993).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M21849; AAA42878.1; -.
DR   EMBL; X65509; CAA46481.1; -.
DR   PIR; JS0321; VGNZCD.
DR   PIR; S21382; S21382.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL       1      ?
FT   CHAIN        ?    662       FUSION GLYCOPROTEIN F0.
FT   CHAIN        ?    224       PROTEIN F2.
FT   CHAIN      225    662       PROTEIN F1.
FT   TRANSMEM   606    629       POTENTIAL.
FT   DISULFID   180    307       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD    62     62       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     3      3       R -> K (IN REF. 2).
FT   CONFLICT   140    140       D -> N (IN REF. 2).
FT   CONFLICT   152    152       N -> S (IN REF. 2).
FT   CONFLICT   171    171       I -> M (IN REF. 2).
FT   CONFLICT   174    174       A -> V (IN REF. 2).
FT   CONFLICT   662    662       L -> H (IN REF. 2).
SQ   SEQUENCE   662 AA;  72970 MW;  FB2C81C9797805F0 CRC64;

  Query Match             65.6%;  Score 59;  DB 1;  Length 662;
  Best Local Similarity   50.0%;  Pred. No. 0.025;
  Matches    9;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|:|||||||:| : :
Db        399 TLSEVKGVIVHRLEAVSY 416


RESULT 5
VGLF_MEASY
ID   VGLF_MEASY     STANDARD;      PRT;   534 AA.
AC   P26032;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Measles virus (strain Yamagata-1) (Subacute sclerose panencephalitis
OS   virus).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11239;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90385702; PubMed=1698327;
RA   Komase K., Haga T., Yoshikawa Y., Sato T.A., Yamanouchi K.;
RT   "Molecular analysis of structural protein genes of the Yamagata-1
RT   strain of defective subacute sclerosing panencephalitis virus. IV.
RT   Nucleotide sequence of the fusion gene.";
RL   Virus Genes 4:173-181(1990).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D10548; BAA01405.1; -.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL       1     23
FT   CHAIN       24    534       FUSION GLYCOPROTEIN F0.
FT   CHAIN       24    112       PROTEIN F2.
FT   CHAIN      113    534       PROTEIN F1.
FT   TRANSMEM   113    136       POTENTIAL.
FT   DOMAIN     137    494       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   495    515       POTENTIAL.
FT   DOMAIN     516    534       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    68    195       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD    29     29       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    61     61       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    67     67       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   534 AA;  57963 MW;  F5B21757B643844D CRC64;

  Query Match             64.4%;  Score 58;  DB 1;  Length 534;
  Best Local Similarity   55.6%;  Pred. No. 0.03;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|||||||||:| : :
Db        287 TLSEIKGVIVHRLEGVSY 304


RESULT 6
VGLF_MEASA
ID   VGLF_MEASA     STANDARD;      PRT;   550 AA.
AC   P35973;
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DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Measles virus (strain AIK-C) (Subacute sclerose panencephalitis
OS   virus).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=36408;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93227570; PubMed=8470368;
RA   Mori T., Sasaki K., Hashimoto H., Makino S.;
RT   "Molecular cloning and complete nucleotide sequence of genomic RNA of
RT   the AIK-C strain of attenuated measles virus.";
RL   Virus Genes 7:67-81(1993).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S58435; AAB26145.1; -.
DR   PIR; E48556; E48556.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL        1     23
FT   CHAIN        24    550       FUSION GLYCOPROTEIN F0.
FT   CHAIN        24    112       PROTEIN F2.
FT   CHAIN       113    550       PROTEIN F1.
FT   TRANSMEM    113    136       POTENTIAL.
FT   DOMAIN      137    494       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    495    515       POTENTIAL.
FT   DOMAIN      516    550       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     68    195       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD     29     29       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     61     61       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     67     67       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   550 AA;  59540 MW;  AAC4DAB92DE0D938 CRC64;

  Query Match             64.4%;  Score 58;  DB 1;  Length 550;
  Best Local Similarity   55.6%;  Pred. No. 0.031;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|||||||||:| : :
Db        287 TLSEIKGVIVHRLEGVSY 304


RESULT 7
VGLF_MEASE
ID   VGLF_MEASE     STANDARD;      PRT;   550 AA.
AC   P08300;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Measles virus (strain Edmonston) (Subacute sclerose panencephalitis
OS   virus),
OS   Measles virus (strain Halle) (Subacute sclerose panencephalitis
OS   virus),
OS   Measles virus (strain Leningrad-16) (Subacute sclerose panencephalitis
OS   virus),
OS   Measles virus (strain Edmonston-Zagreb) (Subacute sclerose
OS   panencephalitis virus),
OS   Measles virus (strain Philadelphia-26) (Subacute sclerose
OS   panencephalitis virus), and
OS   Measles virus (strain Edmonston B) (Subacute sclerose panencephalitis
OS   virus).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11235, 11236, 70147, 70149, 70148, 70146;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Edmonston;
RX   MEDLINE=87071668; PubMed=3788062;
RA   Richardson C.D., Hull D., Greer P., Hasel K., Berkovich A.,
RA   Englund G., Bellini W.J., Rima B., Lazzarini R.A.;
RT   "The nucleotide sequence of the mRNA encoding the fusion protein of
RT   measles virus (Edmonston strain): a comparison of fusion proteins
RT   from several different paramyxoviruses.";
RL   Virology 155:508-523(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Halle;
RX   MEDLINE=87224816; PubMed=3585281;
RA   Buckland R., Gerald C., Barker R., Wild T.F.;
RT   "Fusion glycoprotein of measles virus: nucleotide sequence of the
RT   gene and comparison with other paramyxoviruses.";
RL   J. Gen. Virol. 68:1695-1703(1987).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Edmonston;
RX   MEDLINE=90085790; PubMed=2596022;
RA   Cattaneo R., Schmid A., Spielhofer P., Kaelin K., Baczko K.,
RA   Meulen V., Pardowitz J., Planagan S., Rima B.K., Udem S.A.;
RT   "Mutated and hypermutated genes of persistent measles viruses which
RT   caused lethal human brain diseases.";
RL   Virology 173:415-425(1989).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Edmonston;
RX   MEDLINE=92263801; PubMed=1585658;
RA   Schmid A., Spielhofer P., Cattaneo R., Baczko K., Ter Meulen V.,
RA   Billeter M.A.;
RT   "Subacute sclerosing panencephalitis is typically characterized by
RT   alterations in the fusion protein cytoplasmic domain of the
RT   persisting measles virus.";
RL   Virology 188:910-915(1992).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Edmonston, Leningrad-16, and Edmonston-Zagreb;
RX   MEDLINE=94249283; PubMed=8191786;
RA   Rota J.S., Wang Z.D., Rota P.A., Bellini W.J.;
RT   "Comparison of sequences of the H, F, and N coding genes of measles
RT   virus vaccine strains.";
RL   Virus Res. 31:317-330(1994).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Philadelphia-26;
RX   MEDLINE=94303181; PubMed=8030232;
RA   Hummel K.B., Vanchiere J.A., Bellini W.J.;
RT   "Restriction of fusion protein mRNA as a mechanism of measles virus
RT   persistence.";
RL   Virology 202:665-672(1994).
RN   [7]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Edmonston B;
RA   Billeter M.A.;
RL   Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
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CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M14915; AAA46423.1; -.
DR   EMBL; X05597; CAA29090.1; ALT_INIT.
DR   EMBL; K01711; AAA75498.1; ALT_INIT.
DR   EMBL; K01711; AAA75499.1; -.
DR   EMBL; U03657; AAA56647.1; ALT_INIT.
DR   EMBL; U03659; AAA56649.1; ALT_INIT.
DR   EMBL; U03670; AAA56660.1; ALT_INIT.
DR   EMBL; U08416; AAA50550.1; ALT_INIT.
DR   EMBL; Z66517; CAA91367.1; ALT_INIT.
DR   EMBL; Z66517; CAA91368.1; -.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL       1     23
FT   CHAIN       24    550       FUSION GLYCOPROTEIN F0.
FT   CHAIN       24    112       PROTEIN F2.
FT   CHAIN      113    550       PROTEIN F1.
FT   TRANSMEM   113    136       POTENTIAL.
FT   DOMAIN     137    494       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   495    515       POTENTIAL.
FT   DOMAIN     516    550       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    68    195       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD    29     29       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    61     61       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    67     67       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   550 AA;  59532 MW;  7AA4F1CA82169093 CRC64;

  Query Match             64.4%;  Score 58;  DB 1;  Length 550;
  Best Local Similarity   55.6%;  Pred. No. 0.031;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|||||||||:| : :
Db        287 TLSEIKGVIVHRLEGVSY 304


RESULT 8
VGLF_PHODV
ID   VGLF_PHODV     STANDARD;      PRT;   631 AA.
AC   P28886;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Phocine distemper virus (PDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11240;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Isolate DK88-4A;
RX   MEDLINE=92113538; PubMed=1765768;
RA   Koevamees J., Blixenkrone-Moeller M., Sharma B., Oervell C.,
RA   Norrby E.;
RT   "The nucleotide sequence and deduced amino acid composition of the
RT   haemagglutinin and fusion proteins of the morbillivirus phocid
RT   distemper virus.";
RL   J. Gen. Virol. 72:2959-2966(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Ulster/88;
RX   MEDLINE=92398437; PubMed=1524494;
RA   Curran M.D., Lu Y.J., Rima B.K.;
RT   "The fusion protein gene of phocine distemper virus: nucleotide and
RT   deduced amino acid sequences and a comparison of morbillivirus fusion
RT   proteins.";
RL   Arch. Virol. 126:159-169(1992).
RN   [3]
RP   SEQUENCE OF 95-631 FROM N.A.
RC   STRAIN=Ulster/88;
RX   MEDLINE=91089508; PubMed=2264246;
RA   Curran M.D., Loan D.O., Rima B.K., Kennedy S.;
RT   "Nucleotide sequence analysis of phocine distemper virus reveals its
RT   distinctness from canine distemper virus.";
RL   Vet. Rec. 127:430-431(1990).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D10371; BAA01206.1; -.
DR   PIR; A48346; A48346.
DR   PIR; JQ1368; VGNZPD.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL       1     ?
FT   CHAIN        ?    631       FUSION GLYCOPROTEIN F0.
FT   CHAIN        ?    188       F2 PROTEIN.
FT   CHAIN      194    631       F1 PROTEIN.
FT   DISULFID   149    276       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   TRANSMEM    89    106       POTENTIAL.
FT   TRANSMEM   194    212       POTENTIAL.
FT   TRANSMEM   575    595       POTENTIAL.
FT   CARBOHYD   110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   142    142       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   148    148       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    63     63       I -> V (IN REF. 2).
SQ   SEQUENCE   631 AA;  68873 MW;  D1FC87CDD426E9B8 CRC64;

  Query Match             64.4%;  Score 58;  DB 1;  Length 631;
  Best Local Similarity   44.4%;  Pred. No. 0.035;
  Matches    8;  Conservative    8;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|:|||:|||:| : :
Db        368 TLSEVKGVVVHRLEAVSY 385


RESULT 9
VGLF_RINDK
ID   VGLF_RINDK     STANDARD;      PRT;   546 AA.
AC   P12574;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
```

```
GN   F.
OS   Rinderpest virus (strain Kabete O) (RDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11242;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88322864; PubMed=3413983;
RA   Hsu D., Yamanaka M., Miller J., Dale B., Grubman M., Yilma T.;
RT   "Cloning of the fusion gene of rinderpest virus: comparative sequence
RT   analysis with other morbilliviruses.";
RL   Virology 166:149-153(1988).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M21514; AAA47400.1; -.
DR   PIR; A31051; VGNZRK.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    546       FUSION GLYCOPROTEIN F0.
FT   CHAIN        20    108       F2 PROTEIN.
FT   CHAIN       109    546       F1 PROTEIN.
FT   DOMAIN      104    108       ARG-RICH (BASIC).
FT   TRANSMEM    109    133       POTENTIAL.
FT   TRANSMEM    484    513       POTENTIAL.
FT   DOMAIN      514    517       ARG/LYS-RICH (BASIC).
FT   DISULFID     64    191       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD     25     25       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     57     57       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     63     63       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    518    518       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   546 AA;  58662 MW;  476D74DCC18BCFCF CRC64;

  Query Match             60.0%;  Score 54;  DB 1;  Length 546;
  Best Local Similarity   50.0%;  Pred. No. 0.15;
  Matches    9;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              |::||||||:| :| : :
Db        283 SLSEIKGVIIHALEGVSY 300


RESULT 10
VGLF_MEASI
ID   VGLF_MEASI     STANDARD;      PRT;   529 AA.
AC   P26031; Q83298;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Measles virus (strain IP-3-Ca) (Subacute sclerose panencephalitis
OS   virus).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11237;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92263801; PubMed=1585658;
RA   Schmid A., Spielhofer P., Cattaneo R., Baczko K., Ter Meulen V.,
RA   Billeter M.A.;
RT   "Subacute sclerosing panencephalitis is typically characterized by
RT   alterations in the fusion protein cytoplasmic domain of the
RT   persisting measles virus.";
RL   Virology 188:910-915(1992).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X16566; CAA34567.1; -.
DR   EMBL; X16566; CAA34568.1; ALT_INIT.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL        1     26       BY SIMILARITY.
FT   CHAIN        27    529       FUSION GLYCOPROTEIN F0.
FT   CHAIN        27    115       PROTEIN F2.
FT   CHAIN       116    529       PROTEIN F1.
FT   TRANSMEM    116    139       POTENTIAL.
FT   DOMAIN      140    497       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    498    518       POTENTIAL.
FT   DOMAIN      519    529       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     71    198       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD     32     32       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     64     64       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     70     70       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   529 AA;  57331 MW;  AE987BC9F07E9AA9 CRC64;

  Query Match             55.6%;  Score 50;  DB 1;  Length 529;
  Best Local Similarity   50.0%;  Pred. No. 0.72;
  Matches    9;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::||| ||||:| : :
Db        290 TLSEIKEVIVHRLEGVSY 307


RESULT 11
V725_ARATH
ID   V725_ARATH     STANDARD;      PRT;   220 AA.
AC   O48850;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Vesicle-associated membrane protein 725 (AtVAMP725).
GN   VAMP725 OR AT2G32670 OR F24L7.19.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=20083487; PubMed=10617197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
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RA   Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA   Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA   Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA   Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA   Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
CC   -!- FUNCTION: Involved in the targeting and/or fusion of transport
CC       vesicles to their target membrane (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type IV membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the synaptobrevin family.
CC   -!- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC   -!- SIMILARITY: Contains 1 longin domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AC003974; AAC04496.1; -.
DR   PIR; T00801; T00801.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS50859; LONGIN; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   Transport; Protein transport; Transmembrane; Coiled coil;
KW   Multigene family.
FT   DOMAIN        1    196       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    197    217       ANCHOR FOR TYPE IV MEMBRANE PROTEIN
FT                                (POTENTIAL).
FT   DOMAIN      218    220       VESICULAR (POTENTIAL).
FT   DOMAIN       10    114       LONGIN.
FT   DOMAIN      130    190       V-SNARE COILED-COIL HOMOLOGY.
SQ   SEQUENCE   220 AA;  24938 MW;  F39FBF4A03481DF5 CRC64;

  Query Match             53.3%;  Score 48;  DB 1;  Length 220;
  Best Local Similarity   50.0%;  Pred. No. 0.68;
  Matches    8;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 ITEIKGVIVHRIETIL 18
              :||:|||::  || :|
Db        138 VTEVKGVMMENIEKVL 153


RESULT 12
V726_ARATH
ID   V726_ARATH     STANDARD;      PRT;   229 AA.
AC   Q9MAS5;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Putative vesicle-associated membrane protein 726 (AtVAMP726).
GN   VAMP726 OR AT1G04760 OR F13M7.25.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=21016719; PubMed=11130712;
RA   Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA   White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA   Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA   Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA   Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA   Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA   Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA   Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA   Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA   Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA   Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA   Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA   Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA   Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA   Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA   Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT   "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 408:816-820(2000).
CC   -!- FUNCTION: Involved in the targeting and/or fusion of transport
CC       vesicles to their target membrane (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type IV membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the synaptobrevin family.
CC   -!- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC   -!- SIMILARITY: Contains 1 longin domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AC004809; AAF40460.1; -.
DR   PIR; F86180; F86180.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS50859; LONGIN; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   Hypothetical protein; Transport; Protein transport; Transmembrane;
KW   Coiled coil; Multigene family.
FT   DOMAIN        1    205       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    206    226       ANCHOR FOR TYPE IV MEMBRANE PROTEIN
FT                                (POTENTIAL).
FT   DOMAIN      227    229       VESICULAR (POTENTIAL).
FT   DOMAIN       10    114       LONGIN.
FT   DOMAIN      130    199       V-SNARE COILED-COIL HOMOLOGY.
SQ   SEQUENCE   229 AA;  25867 MW;  E4217AE7EF419E35 CRC64;

  Query Match             53.3%;  Score 48;  DB 1;  Length 229;
  Best Local Similarity   50.0%;  Pred. No. 0.71;
  Matches    8;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 ITEIKGVIVHRIETIL 18
              :||:|||::  || :|
Db        138 VTEVKGVMMENIEKVL 153


RESULT 13
V727_ARATH
ID   V727_ARATH     STANDARD;      PRT;   240 AA.
AC   Q9M376;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Vesicle-associated membrane protein 727 (AtVAMP727).
GN   VAMP727 OR AT3G54300 OR F24B22.260.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
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RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=21016720; PubMed=11130713;
RA   Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
RA   Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA   Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA   De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
RA   Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA   Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA   Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA   Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA   Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA   Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA   Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA   Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA   Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA   de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA   Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA   Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA   Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA   Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA   Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA   Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA   Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA   Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA   Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA   Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA   Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA   Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT   "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 408:820-822(2000).
CC   -!- FUNCTION: Involved in the targeting and/or fusion of transport
CC       vesicles to their target membrane (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type IV membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the synaptobrevin family.
CC   -!- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC   -!- SIMILARITY: Contains 1 longin domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AL132957; CAB71004.1; -.
DR   PIR; T47589; T47589.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS50859; LONGIN; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   Transport; Protein transport; Transmembrane; Coiled coil;
KW   Multigene family.
FT   DOMAIN        1    215       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    216    236       ANCHOR FOR TYPE IV MEMBRANE PROTEIN
FT                                (POTENTIAL).
FT   DOMAIN      237    240       VESICULAR (POTENTIAL).
FT   DOMAIN        6    133       LONGIN.
FT   DOMAIN      149    209       V-SNARE COILED-COIL HOMOLOGY.
SQ   SEQUENCE   240 AA;  27459 MW;  4805B9406E95D47B CRC64;

  Query Match             52.2%;  Score 47;  DB 1;  Length 240;
  Best Local Similarity   50.0%;  Pred. No. 1.1;
  Matches    8;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 ITEIKGVIVHRIETIL 18
              |||:||:::  || :|
Db        157 ITEVKGIMMDNIEKVL 172
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RESULT 14
V721_ARATH
ID   V721_ARATH     STANDARD;      PRT;   219 AA.
AC   Q9ZTW3; O23011; Q9MAS4;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Vesicle-associated membrane protein 721 (AtVAMP721) (v-SNARE
DE   synaptobrevin 7B) (AtVAMP7B).
GN   VAMP721 OR VAMP7B OR AT1G04740/AT1G04750 OR T1G11_1 OR F13M7_23 OR
GN   F13M7.26.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Flower, Rosette leaves, Seedling, Siliques, and Stem;
RA   Nikoloff D.M., Somerville C.R.;
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=21016719; PubMed=11130712;
RA   Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA   White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA   Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA   Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA   Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA   Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA   Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA   Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA   Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA   Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA   Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA   Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA   Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA   Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA   Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA   Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT   "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 408:816-820(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=22954850; PubMed=14593172;
RA   Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA   Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA   Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA   Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA   Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA   Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA   Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA   Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA   Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA   Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA   Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA   Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT   "Empirical analysis of transcriptional activity in the Arabidopsis
RT   genome.";
RL   Science 302:842-846(2003).
CC   -!- FUNCTION: Involved in the targeting and/or fusion of transport
CC       vesicles to their target membrane (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type IV membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the synaptobrevin family.
CC   -!- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC   -!- SIMILARITY: Contains 1 longin domain.
CC   -!- CAUTION: Ref.2 sequences differ from that shown due to erroneous
CC       gene model prediction.
```

```
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AP025333; AAC98905.1; -.
DR   EMBL; AC002376; AAB80624.1; ALT_SEQ.
DR   EMBL; AC004809; AAF40468.1; ALT_SEQ.
DR   EMBL; AY079164; AAL85003.1; -.
DR   EMBL; AY133661; AAM91491.1; -.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS50859; LONGIN; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   Transport; Protein transport; Transmembrane; Coiled coil;
KW   Multigene family.
FT   DOMAIN        1    196       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    197    217       ANCHOR FOR TYPE IV MEMBRANE PROTEIN
FT                                (POTENTIAL).
FT   DOMAIN      218    219       VESICULAR (POTENTIAL).
FT   DOMAIN       10    114       LONGIN.
FT   DOMAIN      130    190       V-SNARE COILED-COIL HOMOLOGY.
SQ   SEQUENCE   219 AA;  24765 MW;  7F234F6DB5138082 CRC64;

  Query Match             48.9%;  Score 44;  DB 1;  Length 219;
  Best Local Similarity   43.8%;  Pred. No. 3.3;
  Matches    7;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 ITEIKGVIVHRIETIL 18
              ::|:|||::  || :|
Db        138 VSEVKGVMMENIEKVL 153


RESULT 15
V722_ARATH
ID   V722_ARATH     STANDARD;      PRT;   221 AA.
AC   P47192; O49321;
DT   01-NOV-1995 (Rel. 32, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Vesicle-associated membrane protein 722 (AtVAMP722) (Synaptobrevin-
DE   related protein 1).
GN   VAMP722 OR SAR1 OR HAT24 OR AT2G33120 OR F25I18.14.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RA   Schena M., Davis R.W.;
RT   "The SAR1 gene of Arabidopsis thaliana encodes a member of
RT   synaptobrevin family of membrane proteins.";
RL   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=20083487; PubMed=10617197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA   Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA   Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA   Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA   Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA   Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA   Feldmann K.A.;
RT   "Full-length cDNA from Arabidopsis thaliana.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=22954850; PubMed=14593172;
RA   Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA   Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA   Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA   Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA   Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA   Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA   Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA   Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA   Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA   Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA   Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA   Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT   "Empirical analysis of transcriptional activity in the Arabidopsis
RT   genome.";
RL   Science 302:842-846(2003).
RN   [5]
RP   SEQUENCE OF 140-200 FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=92237275; PubMed=1349174;
RA   Schena M., Davis R.W.;
RT   "HD-Zip proteins: members of an Arabidopsis homeodomain protein
RT   superfamily.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:3894-3898(1992).
CC   -!- FUNCTION: Involved in the targeting and/or fusion of transport
CC       vesicles to their target membrane (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type IV membrane protein (Probable).
CC   -!- SIMILARITY: Belongs to the synaptobrevin family.
CC   -!- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC   -!- SIMILARITY: Contains 1 longin domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M90418; AAA56991.1; -.
DR   EMBL; AC002334; AAC04921.1; -.
DR   EMBL; AY086363; AAM64431.1; -.
DR   EMBL; AY072422; AAL62414.1; -.
DR   EMBL; AF419564; AAL31896.1; -.
DR   EMBL; AY079037; AAL79587.1; -.
DR   EMBL; AY114706; AAM48025.1; -.
DR   EMBL; AY128288; AAM91096.1; -.
DR   PIR; F84741; F84741.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS50859; LONGIN; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   Transport; Protein transport; Transmembrane; Coiled coil;
KW   Multigene family.
FT   DOMAIN        1    196       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    197    217       ANCHOR FOR TYPE IV MEMBRANE PROTEIN
FT                                (POTENTIAL).
```

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FT   DOMAIN      218    221       VESICULAR (POTENTIAL).
FT   DOMAIN       10    114       LONGIN.
FT   DOMAIN      130    190       V-SNARE COILED-COIL HOMOLOGY.
FT   CONFLICT    123    123       D -> A (IN REF. 1).
SQ   SEQUENCE   221 AA;  24928 MW;  880AA7BA2C24697B CRC64;

  Query Match             48.9%;  Score 44;  DB 1;  Length 221;
  Best Local Similarity   43.8%;  Pred. No. 3.4;
  Matches    7;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 ITEIKGVIVHRIETIL 18
              ::|:|||::  || :|
Db        138 VSEVKGVMMENIEKVL 153


Search completed: June 18, 2004, 19:59:36
Job time : 4.73006 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:15 ; Search time 18.4172 Seconds
(without alignments)
325.503 Million cell updates/sec

Title: US-09-865-294A-51
Perfect score: 90
Sequence: 1 ISITEIKGVIVHRIETILF 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	61	67.8	546	12	Q91HA5	Q91ha5 rinderpest
2	60	66.7	546	12	Q84926	Q84926 peste-des-p
3	59	65.6	528	12	Q9YJW9	Q9yjw9 canine dist
4	59	65.6	530	12	Q8QV06	Q8qv06 canine dist
5	59	65.6	552	12	Q66147	Q66147 cetacean mo
6	59	65.6	662	12	Q9DXZ2	Q9dxz2 canine dist
7	59	65.6	662	12	Q91KN3	Q91kn3 canine dist
8	59	65.6	662	12	Q9YKL7	Q9ykl7 canine dist
9	59	65.6	662	12	O89327	O89327 canine dist
10	58	64.4	534	12	Q04243	Q04243 measles vir
11	58	64.4	537	12	Q04242	Q04242 measles vir
12	58	64.4	545	12	Q9PXA4	Q9pxa4 measles vir
13	58	64.4	550	12	P90331	P90331 measles vir
14	58	64.4	550	12	Q9QEX0	Q9qex0 measles vir
15	58	64.4	550	12	Q9QEW9	Q9qew9 measles vir
16	58	64.4	550	12	P90330	P90330 measles vir
17	58	64.4	550	12	Q9QEW7	Q9qew7 measles vir
18	58	64.4	550	12	Q9WMK4	Q9wmk4 measles vir
19	58	64.4	550	12	Q89495	Q89495 measles vir
20	58	64.4	550	12	Q8V049	Q8v049 measles vir
21	58	64.4	550	12	Q9YJ94	Q9yj94 measles vir
22	58	64.4	550	12	Q9QEX1	Q9qex1 measles vir
23	58	64.4	550	12	Q9QEW8	Q9qew8 measles vir
24	58	64.4	553	12	O93055	O93055 measles vir
25	58	64.4	553	12	Q9IC36	Q9ic36 measles vir
26	58	64.4	553	12	P88973	P88973 measles vir
27	58	64.4	553	12	Q83536	Q83536 measles vir
28	58	64.4	553	12	O11383	O11383 measles vir
29	58	64.4	553	12	Q9IFK2	Q9ifk2 measles vir
30	58	64.4	553	12	Q83533	Q83533 measles vir
31	58	64.4	553	12	Q83525	Q83525 measles vir
32	58	64.4	553	12	Q83518	Q83518 measles vir
33	58	64.4	553	12	P88974	P88974 measles vir
34	58	64.4	553	12	Q83527	Q83527 measles vir
35	58	64.4	553	12	Q83521	Q83521 measles vir
36	58	64.4	553	12	Q83530	Q83530 measles vir
37	58	64.4	553	12	O91248	O91248 measles vir
38	58	64.4	553	12	Q91QP2	Q91qp2 measles vir
39	58	64.4	553	12	Q04244	Q04244 measles vir
40	58	64.4	579	12	Q9PWU4	Q9pwu4 measles vir
41	56	62.2	552	12	Q66409	Q66409 dolphin mor
42	56	62.2	552	12	O56852	O56852 dolphin mor
43	56	62.2	553	12	O11380	O11380 measles vir
44	54	60.0	545	12	Q9QEW6	Q9qew6 measles vir
45	48	53.3	285	10	Q8GXC1	Q8gxc1 arabidopsis

ALIGNMENTS

RESULT 1
Q91HA5
ID Q91HA5 PRELIMINARY; PRT; 546 AA.
AC Q91HA5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fusion protein.
GN F.
OS Rinderpest virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K;
RX MEDLINE=21014265; PubMed=11186456;
RA Aiańot P.K., Sminev A.G., Bezborodova S.V., Starov S.K., Drygin V.V.,
RA Gusev A.A.;
RT "Primary structure of the F-gene from Rinderpest virus strain K.";
RL Mol. Gen. Mikrobiol. Virusol. 4:29-33(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K;
RA Ayanot P.K., Sminev A.G., Bezborodova S.V., Starov S.K., Drygin V.V.,
RA Gusev A.A.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY035887; AAK63190.1; -.
DR PIR; PQ0866; PQ0866.
DR PIR; PQ0867; PQ0867.
DR PIR; PQ0873; PQ0873.
DR GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
SQ SEQUENCE 546 AA; 58572 MW; 449B2B2DD7405F0B CRC64;

Query Match 67.8%; Score 61; DB 12; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.094;

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  Matches   11;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
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Db        283 SLSEIKGVIVHRLEGVSY 300


RESULT 2
Q84926
ID   Q84926      PRELIMINARY;      PRT;   546 AA.
AC   Q84926;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fusion protein.
GN   F.
OS   Peste-des-petits-ruminants virus (PPRV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=31604;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VACCINE STRAIN;
RX   MEDLINE=96082318; PubMed=7483819;
RA   Meyer G., Diallo A.;
RT   "The nucleotide sequence of fusion protein gene of the Peste des
RT   petits ruminants virus: the long untranslated region in the 5'end of
RT   the F gene of morbilliviruses seems to be specific to each virus.";
RL   Virus Res. 37:23-35(1995).
DR   EMBL; Z37017; CAA85451.1; -.
DR   PIR; S55386; S55386.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
SQ   SEQUENCE   546 AA;  59310 MW;  DF7D903A4048A0BB CRC64;

  Query Match             66.7%;  Score 60;  DB 12;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 0.14;
  Matches   11;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|||||||:|| | :
Db        283 TLSEIKGVIVHKIEAISY 300


RESULT 3
Q9YJW9
ID   Q9YJW9      PRELIMINARY;      PRT;   528 AA.
AC   Q9YJW9;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fusion protein precursor (Fragment).
GN   F.
OS   Canine distemper virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11232;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2544/Han95, and CV. 5th passage Vero;
RA   Liermann H., Harder T.C., Loechelt M., Baumgaertner W., Moennig V.,
RA   Haas L.;
RT   "Genetic analysis of the central untranslated genome region and the
RT   proximal coding part of the F gene of wild-type and vaccine canine
RT   distemper morbilliviruses.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2544/Han95, and CV. 5th passage Vero;
RA   Harder T.C., von Messling V., Oervell C., Moennig V., Haas L.;
RT   "Wild-type canine distemper virus nucleocapsid, fusion and
RT   hemagglutinin protein expression in recombinant baculovirus.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ007711; CAA07617.1; -.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Signal.
FT   NON_TER       1      1
FT   SIGNAL        <1     10       POTENTIAL.
FT   CHAIN         11    >528      FUSION PROTEIN.
FT   NON_TER      528     528
SQ   SEQUENCE   528 AA;  57613 MW;  146CBCFBF6EF6516 CRC64;

  Query Match             65.6%;  Score 59;  DB 12;  Length 528;
  Best Local Similarity   50.0%;  Pred. No. 0.2;
  Matches    9;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|:|||||||:| : :
Db        272 TLSEVKGVIVHRLEAVSY 289


RESULT 4
Q8QV06
ID   Q8QV06      PRELIMINARY;      PRT;   530 AA.
AC   Q8QV06;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fusion protein (Fragment).
GN   F.
OS   Canine distemper virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11232;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DOG/DK 91C;
RA   Andersen M.K.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF355188; AAL83966.1; -.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   530 AA;  57985 MW;  8F7173C247AF233D CRC64;

  Query Match             65.6%;  Score 59;  DB 12;  Length 530;
  Best Local Similarity   50.0%;  Pred. No. 0.2;
  Matches    9;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|:|||||||:| : :
Db        267 TLSEVKGVIVHRLEAVSY 284


RESULT 5
Q66147
ID   Q66147      PRELIMINARY;      PRT;   552 AA.
AC   Q66147;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fusion protein precursor.
OS   Cetacean morbillivirus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=36410;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RC   STRAIN=porpoise;
RX   MEDLINE=95159670; PubMed=7531923;
RA   Bolt G.G.B., Blixenkrone-Moller M.M.B., Gottschalck E., Wishaupt R.G.,
RA   Welsh M.J., Earle J.A.P., Rima B.K.;
RT   "Nucleotide and deduced amino acid sequences of the matrix (M) and
RT   fusion (F) protein genes of cetacean morbilliviruses isolated from a
RT   porpoise and a dolphin.";
RL   Virus Res. 34:291-304(1994).
DR   EMBL; X80757; CAA56731.1; -.
DR   PIR; S47034; S47034.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Signal.
FT   SIGNAL        1     25       POTENTIAL.
SQ   SEQUENCE   552 AA;  60025 MW;  40D9191AD910EA1E CRC64;

  Query Match             65.6%;  Score 59;  DB 12;  Length 552;
  Best Local Similarity   50.0%;  Pred. No. 0.21;
  Matches    9;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|:|||||||:| : :
Db        289 TLSEVKGVIVHRLEAVSY 306


RESULT 6
Q9DXZ2
ID   Q9DXZ2      PRELIMINARY;      PRT;   662 AA.
AC   Q9DXZ2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fusion protein F.
OS   Canine distemper virus (strain Onderstepoort) (CDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11233;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Onderstepoort;
RX   MEDLINE=20499096; PubMed=11044118;
RA   Gassen U., Collins F.M., Duprex W.P., Rima B.K.;
RT   "Establishment of a rescue system for canine distemper virus.";
RL   J. Virol. 74:10737-10744(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Onderstepoort;
RA   Gassen U., Collins F.M., Duprex P., Rima B.K.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF305419; AAG30919.1; -.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
SQ   SEQUENCE   662 AA;  72988 MW;  9C5C1398C8AE7B4C CRC64;

  Query Match             65.6%;  Score 59;  DB 12;  Length 662;
  Best Local Similarity   50.0%;  Pred. No. 0.25;
  Matches    9;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|:|||||||:| : :
Db        399 TLSEVKGVIVHRLEAVSY 416


RESULT 7
Q91KN3
ID   Q91KN3      PRELIMINARY;      PRT;   662 AA.
AC   Q91KN3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fusion protein F.
OS   Canine distemper virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11232;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21306344; PubMed=11413309;
RA   von Messling V., Zimmer G., Herrler G., Haas L., Cattaneo R.;
RT   "The hemagglutinin of canine distemper virus determines tropism and
RT   cytopathogenicity.";
RL   J. Virol. 75:6418-6427(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   von Messling V.A., Zimmer G., Herrler G., Haas L., Cattaneo R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF378705; AAK54668.1; -.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
SQ   SEQUENCE   662 AA;  72898 MW;  CC6A104A96BBF8A0 CRC64;

  Query Match             65.6%;  Score 59;  DB 12;  Length 662;
  Best Local Similarity   50.0%;  Pred. No. 0.25;
  Matches    9;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|:|||||||:| : :
Db        399 TLSEVKGVIVHRLEAVSY 416


RESULT 8
Q9YKL7
ID   Q9YKL7      PRELIMINARY;      PRT;   662 AA.
AC   Q9YKL7;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fusion protein.
GN   F.
OS   Canine distemper virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11232;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A75/17;
RX   MEDLINE=99139009; PubMed=9971809;
RA   Cherpillod P., Beck K., Zurbriggen A., Wittek R.;
RT   "Sequence analysis and expression of the attachment and fusion
RT   proteins of canine distemper virus wild-type strain A75/17.";
RL   J. Virol. 73:2263-2269(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A75/17;
RA   Wiederkehr C., Howley P., Zurbriggen A., Wittek R.;
RT   "Complete sequence of canine distemper wildtype strain A75/17.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF112188; AAD18007.1; -.
DR   EMBL; AF164967; AAD49702.1; -.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
SQ   SEQUENCE   662 AA;  72537 MW;  68F992DCBA51F0BA CRC64;

  Query Match             65.6%;  Score 59;  DB 12;  Length 662;
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  Best Local Similarity   50.0%;  Pred. No. 0.25;
  Matches    9;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|:|||||||:| : :
Db        399 TLSEVKGVIVHRLEAVSY 416


RESULT 9
O89327
ID   O89327      PRELIMINARY;      PRT;   662 AA.
AC   O89327;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fusion protein F.
OS   Canine distemper virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11232;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Onderstpoort;
RX   MEDLINE=93174978; PubMed=8438593;
RA   Sidhu M.S., Husar W., Cook S.D., Dowling P.C., Udem S.A.;
RT   "Canine distemper terminal and intergenic non-protein coding
RT   nucleotide sequences: completion of the entire CDV genome sequence.";
RL   Virology 193:66-72(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Onderstpoort;
RA   Sidhu M.;
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF014953; AAC26994.1; -.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
SQ   SEQUENCE   662 AA;  72951 MW;  80B144C6B9801898 CRC64;

  Query Match             65.6%;  Score 59;  DB 12;  Length 662;
  Best Local Similarity   50.0%;  Pred. No. 0.25;
  Matches    9;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|:|||||||:| : :
Db        399 TLSEVKGVIVHRLEAVSY 416


RESULT 10
Q04243
ID   Q04243      PRELIMINARY;      PRT;   534 AA.
AC   Q04243;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fusion protein.
GN   F.
OS   Measles virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11234;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89003063; PubMed=3167982;
RA   Cattaneo R., Schmid A., Eschle D., Baczko K., ter Meulen V.,
RA   Billeter M.A.;
RT   "Biased hypermutation and other genetic changes in defective measles
RT   viruses in human brain infections.";
RL   Cell 55:255-265(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Cattaneo R., Billeter M.A.;
RL   Virology 0:0-0(0).
DR   EMBL; X16568; CAA34581.1; -.
DR   EMBL; X16568; CAA34582.1; -.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
SQ   SEQUENCE   534 AA;  57899 MW;  637245E23B5BE044 CRC64;

  Query Match             64.4%;  Score 58;  DB 12;  Length 534;
  Best Local Similarity   55.6%;  Pred. No. 0.3;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|||||||||:| : :
Db        290 TLSEIKGVIVHRLEGVSY 307


RESULT 11
Q04242
ID   Q04242      PRELIMINARY;      PRT;   537 AA.
AC   Q04242;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fusion protein.
GN   F.
OS   Measles virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11234;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89003063; PubMed=3167982;
RA   Cattaneo R., Schmid A., Eschle D., Baczko K., ter Meulen V.,
RA   Billeter M.A.;
RT   "Biased hypermutation and other genetic changes in defective measles
RT   viruses in human brain infections.";
RL   Cell 55:255-265(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Cattaneo R., Billeter M.A.;
RL   Virology 0:0-0(0).
DR   EMBL; X16567; CAA34574.1; -.
DR   EMBL; X16567; CAA34575.1; -.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
SQ   SEQUENCE   537 AA;  58275 MW;  D0A60AC66D979E06 CRC64;

  Query Match             64.4%;  Score 58;  DB 12;  Length 537;
  Best Local Similarity   55.6%;  Pred. No. 0.3;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::|||||||||:| : :
Db        290 TLSEIKGVIVHRLEGVSY 307


RESULT 12
Q9PXA4
ID   Q9PXA4      PRELIMINARY;      PRT;   545 AA.
AC   Q9PXA4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fusion protein.
OS   Measles virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
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OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OSA-3;
RA   Ning X., Ayata M., Morimoto K., Ito N., Shingai M., Kimura M.,
RA   Ogura H.;
RT   "Nucleotide sequences of the fusion protein gene of subacute
RT   sclerosing panencephalitis viruses: deduced amino acid sequences
RT   showed the cytoplasmic domain highly mutated --truncated, elongated or
RT   predicted secondary structure changed.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF179440; AAF02705.1; -.
DR   EMBL; AF179439; AAF02704.1; -.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
SQ   SEQUENCE   545 AA;  58907 MW;  0234C28AE193E77D CRC64;

  Query Match             64.4%;  Score 58;  DB 12;  Length 545;
  Best Local Similarity   55.6%;  Pred. No. 0.31;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILP 19
              :::|||||||||:| : :
Db        287 TLSEIKGVIVHRLEGVSY 304


RESULT 13
P90331
ID   P90331      PRELIMINARY;      PRT;   550 AA.
AC   P90331;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fusion protein.
GN   F.
OS   Measles virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NAGAHATA;
RA   Sheng J., Watanabe M., Ueda S.;
RT   "Selection of a neurotropic variant of measles virus.";
RL   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NAGAHATA;
RA   Sheng J., Nakanishi M., Watanabe M., Ueda S.;
RT   "An amino acid alteration of F protein responsible for the enhanced
RT   fusogenicity of measles virus.";
RL   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NAGAHATA;
RA   Ning X., Ayata M., Morimoto K., Ito N., Shingai M., Kimura M.,
RA   Ogura H.;
RT   "Nucleotide sequences of the fusion protein gene of subacute
RT   sclerosing panencephalitis viruses: deduced amino acid sequences
RT   showed the cytoplasmic domain highly mutated --truncated, elongated or
RT   predicted secondary structure changed.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; D63926; BAA09958.1; -.
DR   EMBL; AF179431; AAF02696.1; -.
DR   PIR; PQ0376; PQ0376.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
SQ   SEQUENCE   550 AA;  59530 MW;  97C991C7E2169839 CRC64;

  Query Match             64.4%;  Score 58;  DB 12;  Length 550;
  Best Local Similarity   55.6%;  Pred. No. 0.31;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILP 19
              :::|||||||||:| : :
Db        287 TLSEIKGVIVHRLEGVSY 304


RESULT 14
Q9QEX0
ID   Q9QEX0      PRELIMINARY;      PRT;   550 AA.
AC   Q9QEX0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fusion protein.
OS   Measles virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Toyoshima;
RA   Ning X., Ayata M., Morimoto K., Ito N., Shingai M., Kimura M.,
RA   Ogura H.;
RT   "Nucleotide sequences of the fusion protein gene of subacute
RT   sclerosing panencephalitis viruses: deduced amino acid sequences
RT   showed the cytoplasmic domain highly mutated --truncated, elongated or
RT   predicted secondary structure changed.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF179432; AAF02697.1; -.
DR   PIR; PQ0376; PQ0376.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
SQ   SEQUENCE   550 AA;  59504 MW;  2AA969D37FA5CA17 CRC64;

  Query Match             64.4%;  Score 58;  DB 12;  Length 550;
  Best Local Similarity   55.6%;  Pred. No. 0.31;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILP 19
              :::|||||||||:| : :
Db        287 TLSEIKGVIVHRLEGVSY 304


RESULT 15
Q9QEW9
ID   Q9QEW9      PRELIMINARY;      PRT;   550 AA.
AC   Q9QEW9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fusion protein.
OS   Measles virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OSA-2;
RA   Ning X., Ayata M., Morimoto K., Ito N., Shingai M., Kimura M.,
RA   Ogura H.;
RT   "Nucleotide sequences of the fusion protein gene of subacute
RT   sclerosing panencephalitis viruses: deduced amino acid sequences
RT   showed the cytoplasmic domain highly mutated --truncated, elongated or
RT   predicted secondary structure changed.";
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```
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF179436; AAF02701.1; -.
DR   PIR; PQ0376; PQ0376.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
SQ   SEQUENCE   550 AA;  59405 MW;  0AE6DBFC5DD22BBA CRC64;

  Query Match             64.4%;  Score 58;  DB 12;  Length 550;
  Best Local Similarity   55.6%;  Pred. No. 0.31;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 SITEIKGVIVHRIETILF 19
              :::||||||||:| : :
Db        287 TLSEIKGVIVHRLEGVSY 304


Search completed: June 18, 2004, 20:02:28
Job time : 20.4172 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:20 ; Search time 43.2515 Seconds
(without alignments)
195.980 Million cell updates/sec

Title: US-09-865-294A-71
Perfect score: 152
Sequence: 1 DAEFRHDSGYKISITEIKGVIVHRIETILF 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	152	100.0	30	6	AAE35677	Aae35677 Human Abe
2	141	92.8	32	6	AAE35678	Aae35678 Human Abe
3	140	92.1	34	6	AAE35679	Aae35679 Human Abe
4	133	87.5	48	6	AAE35680	Aae35680 Human Abe
5	126	82.9	34	6	AAE35681	Aae35681 Human Abe
6	119	78.3	34	6	AAE35682	Aae35682 Human Abe
7	90	59.2	19	6	AAE35657	Aae35657 Measles v
8	90	59.2	31	7	ADD89946	Add89946 CD4 pepti
9	90	59.2	45	7	ADD89951	Add89951 IgE pepti
10	90	59.2	50	7	ADD89944	Add89944 CD4 pepti
11	87	57.2	65	7	ADD89953	Add89953 Foot-and-
12	83	54.6	65	7	ADD89952	Add89952 Foot-and-
13	80.5	53.0	31	3	AAY91268	Aay91268 Modified
14	78	51.3	29	3	AAY91260	Aay91260 Modified
15	76	50.0	19	3	AAY68551	Aay68551 Helper T
16	76	50.0	19	3	AAY91135	Aay91135 Modified
17	76	50.0	19	5	ABG68202	Abg68202 Measles v
18	76	50.0	19	5	ABG68208	Abg68208 Measles v
19	76	50.0	19	6	AAE35653	Aae35653 Measles v
20	76	50.0	19	6	AAE35647	Aae35647 Measles v
21	76	50.0	19	6	AAE35644	Aae35644 Measles v
22	76	50.0	29	3	AAY91264	Aay91264 Modified
23	76	50.0	29	3	AAY91266	Aay91266 Modified
24	76	50.0	29	3	AAY91258	Aay91258 Modified
25	76	50.0	30	3	AAY91262	Aay91262 Modified
26	76	50.0	30	5	ABG68233	Abg68233 Optimised
27	76	50.0	31	3	AAY68582	Aay68582 Peptide i
28	76	50.0	31	3	AAY91173	Aay91173 Modified
29	76	50.0	32	5	ABG68235	Abg68235 Optimised
30	76	50.0	34	5	ABG68231	Abg68231 Optimised
31	76	50.0	35	3	AAY91242	Aay91242 Modified
32	76	50.0	36	3	AAY91224	Aay91224 Modified
33	76	50.0	36	3	AAY91234	Aay91234 Modified
34	76	50.0	36	3	AAY91238	Aay91238 Modified
35	76	50.0	39	5	ABG68237	Abg68237 Optimised
36	76	50.0	46	3	AAY91240	Aay91240 Modified
37	76	50.0	46	3	AAY91213	Aay91213 Modified
38	76	50.0	46	3	AAY91232	Aay91232 Modified
39	76	50.0	46	3	AAY80020	Aay80020 IgE immun
40	76	50.0	46	5	ABG68229	Abg68229 Optimised
41	76	50.0	46	5	ABG68227	Abg68227 Optimised
42	76	50.0	47	3	AAY68583	Aay68583 Peptide i
43	76	50.0	47	3	AAY91180	Aay91180 Inv epito
44	76	50.0	49	3	AAY91177	Aay91177 Modified
45	76	50.0	51	3	AAY91248	Aay91248 Modified

ALIGNMENTS

RESULT 1
AAE35677
ID AAE35677 standard; peptide; 30 AA.
XX
AC AAE35677;
XX
DT 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)
XX
DE Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #1.
XX
KW Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS Homo sapiens.
OS Measles virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1. .10
FT /note= "Human beta amyloid peptide"
FT Region 14. .30
FT /note= "Measles virus T helper cell epitope"
XX
PN WO200296350-A2.
XX
PD 05-DEC-2002.
XX
PF 02-APR-2002; 2002WO-US010293.
XX
PR 25-MAY-2001; 2001US-00865294.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2003-201258/19.
XX
PT Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.
XX
PS Claim 9; Page 39; 77pp; English.
XX
CC The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a

```
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 30 AA;

  Query Match             100.0%;  Score 152;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-16;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYKISITEIKGVIVHRIETILP 30
              ||||||||||||||||||||||||||||||
Db          1 DAEFRHDSGYKISITEIKGVIVHRIETILP 30


RESULT 2
AAE35678
ID   AAE35678 standard; peptide; 32 AA.
XX
AC   AAE35678;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #2.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .12
FT                   /note= "Human beta amyloid peptide"
FT   Region          16. .32
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Claim 9; Page 39; 77pp; English.
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 32 AA;

  Query Match             92.8%;  Score 141;  DB 6;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 8.3e-15;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGY--KISITEIKGVIVHRIETILP 30
              ||||||||||  ||||||||||||||||||||
Db          1 DAEFRHDSGYEVKISITEIKGVIVHRIETILP 32


RESULT 3
AAE35679
ID   AAE35679 standard; peptide; 34 AA.
XX
AC   AAE35679;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #3.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .14
FT                   /note= "Human beta amyloid peptide"
FT   Region          18. .34
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Claim 9; Page 39; 77pp; English.
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```
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 34 AA;

  Query Match             92.1%;  Score 140;  DB 6;  Length 34;
  Best Local Similarity   88.2%;  Pred. No. 1.3e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    4;  Gaps    1;

Qy          1 DAEFRHDSGY----KISITEIKGVIVHRIETILF 30
              ||||||||||    ||||||||||||||||||||
Db          1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34


RESULT 4
AAE35680
ID   AAE35680 standard; peptide; 48 AA.
XX
AC   AAE35680;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #4.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .28
FT                   /note= "Human beta amyloid peptide"
FT   Region          32. .48
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Claim 9; Page 39; 77pp; English.
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 48 AA;

  Query Match             87.5%;  Score 133;  DB 6;  Length 48;
  Best Local Similarity   62.5%;  Pred. No. 2.5e-13;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels   18;  Gaps    1;

Qy          1 DAEFRHDSGY------------------KISITEIKGVIVHRIETILF 30
              ||||||||||                  ||||||||||||||||||||
Db          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48


RESULT 5
AAE35681
ID   AAE35681 standard; peptide; 34 AA.
XX
AC   AAE35681;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #5.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .14
FT                   /note= "Human beta amyloid peptide"
FT   Region          18. .34
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
```

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PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Disclosure; Page 39; 77pp; English.
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 34 AA;

  Query Match             82.9%;  Score 126;  DB 6;  Length 34;
  Best Local Similarity   79.4%;  Pred. No. 2.1e-12;
  Matches   27;  Conservative    2;  Mismatches    1;  Indels    4;  Gaps    1;

Qy          1 DAEFRHDSGY----KISITEIKGVIVHRIETILF 30
              ||||||||||    ||||:|||||||:|| |||
Db          1 DAEFRHDSGYEVHHKISISEIKGVIVHKIEGILF 34


RESULT 6
AAE35682
ID   AAE35682 standard; peptide; 34 AA.
XX
AC   AAE35682;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #6.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .14
FT                   /note= "Human beta amyloid peptide"
FT   Region          18. .34
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Disclosure; Page 39; 77pp; English.
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 34 AA;

  Query Match             78.3%;  Score 119;  DB 6;  Length 34;
  Best Local Similarity   79.4%;  Pred. No. 2.6e-11;
  Matches   27;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy          1 DAEFRHDSGY----KISITEIKGVIVHRIETILF 30
              ||||||||||    |||||||: ||| |||||||
Db          1 DAEFRHDSGYEVHHKISITEIRTVIVTRIETILF 34


RESULT 7
AAE35657
ID   AAE35657 standard; peptide; 19 AA.
XX
AC   AAE35657;
XX
DT   17-JUN-2003  (first entry)
XX
DE   Measles virus T helper cell epitope #31.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic.
XX
OS   Measles virus.
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Claim 1; Page 37; 77pp; English.
XX
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CC The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is measles virus T helper (Th) cell epitope used in the
CC exemplification of the invention
XX
SQ Sequence 19 AA;

Query Match 59.2%; Score 90; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.5e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ISITEIKGVIVHRIETILF 30
||||||||||||||||||||
Db 1 ISITEIKGVIVHRIETILF 19

RESULT 8
ADD89946
ID ADD89946 standard; protein; 31 AA.
XX
AC ADD89946;
XX
DT 29-JAN-2004 (first entry)
XX
DE CD4 peptide used in immunostimulant complex for anti-HIV vaccine.
XX
KW Immunostimulant; vaccine; human; immunogen; anti-HIV; immunotherapy; CD4.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 20
FT /note= "Epsilon-lysine"
XX
PN WO2003068169-A2.
XX
PD 21-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-US004711.
XX
PR 14-FEB-2002; 2002US-00076674.
PR 31-JAN-2003; 2003US-00076674.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Sokoll KK;
XX
DR WPI; 2003-778890/73.
XX
PT Stabilized immunostimulating complex, useful for vaccination, e.g.
PT against human immune deficiency viruses, comprises cationic peptide
PT immunogen and anionic oligonucleotide.
XX
PS Claim 14; SEQ ID NO 6; 159pp; English.
XX
CC The present sequence is that of a synthetic immunogenic peptide derived
CC from human CD4. This is an example of peptides that can be used in
CC claimed immunostimulatory complexes of the invention that are
CC specifically adapted to act as adjuvant and as peptide immunogen
CC stabiliser. The complexes comprise a CpG oligonucleotide and a
CC biologically active peptide immunogen. The complex is particulate and can
CC efficiently present peptide immunogens to the cells of the immune system
CC to produce an immune response. The complexes may be prepared with various
CC ratios of peptides to CpG oligonucleotides to provide different physical
CC properties, such as the size of the microparticle. An immunostimulatory
CC complex comprising the present CD4 derived peptide can be used in an anti
CC -CD4 immunotherapeutic vaccine for the treatment of HIV infection.
XX
SQ Sequence 31 AA;

Query Match 59.2%; Score 90; DB 7; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.5e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ISITEIKGVIVHRIETILF 30
||||||||||||||||||||
Db 1 ISITEIKGVIVHRIETILF 19

RESULT 9
ADD89951
ID ADD89951 standard; protein; 45 AA.
XX
AC ADD89951;
XX
DT 29-JAN-2004 (first entry)
XX
DE IgE peptide used in immunostimulant complex for allergy vaccine.
XX
KW Immunostimulant; vaccine; human; immunogen; IgE; immunotherapy; allergy;
KW antibody; antiallergic.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 20
FT /note= "Epsilon-lysine"
XX
PN WO2003068169-A2.
XX
PD 21-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-US004711.
XX
PR 14-FEB-2002; 2002US-00076674.
PR 31-JAN-2003; 2003US-00076674.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Sokoll KK;
XX
DR WPI; 2003-778890/73.
XX
PT Stabilized immunostimulating complex, useful for vaccination, e.g.
PT against human immune deficiency viruses, comprises cationic peptide
PT immunogen and anionic oligonucleotide.
XX
PS Claim 20; SEQ ID NO 11; 159pp; English.
XX
CC The present sequence is that of a synthetic immunogenic peptide derived
CC from human IgE. This is an example of peptides that can be used in
CC claimed immunostimulatory complexes of the invention that are
CC specifically adapted to act as adjuvant and as peptide immunogen
CC stabiliser. The complexes comprise a CpG oligonucleotide and a
CC biologically active peptide immunogen. The complex is particulate and can
CC efficiently present peptide immunogens to the cells of the immune system
CC to produce an immune response. The complexes may be prepared with various
CC ratios of peptides to CpG oligonucleotides to provide different physical
CC properties, such as the size of the microparticle. An immunostimulatory
CC complex comprising the present IgE derived peptide can be used in an anti
CC -IgE immunotherapeutic vaccine for the treatment of allergy.

```
XX
SQ   Sequence 45 AA;

  Query Match             59.2%;  Score 90;  DB 7;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 10
ADD89944
ID   ADD89944 standard; protein; 50 AA.
XX
AC   ADD89944;
XX
DT   29-JAN-2004  (first entry)
XX
DE   CD4  peptide used in immunostimulant complex as anti-HIV vaccine.
XX
KW   Immunostimulant; vaccine; human; immunogen; anti-HIV; immunotherapy.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   20
FT                   /note= "Epsilon-lysine"
XX
PN   WO2003068169-A2.
XX
PD   21-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004711.
XX
PR   14-FEB-2002; 2002US-00076674.
PR   31-JAN-2003; 2003US-00076674.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Sokoll KK;
XX
DR   WPI; 2003-778890/73.
XX
PT   Stabilized immunostimulating complex, useful for vaccination, e.g.
PT   against human immune deficiency viruses, comprises cationic peptide
PT   immunogen and anionic oligonucleotide.
XX
PS   Claim 14; SEQ ID NO 4; 159pp; English.
XX
CC   The present sequence is that of a synthetic immunogenic peptide derived
CC   from human CD4. This is an example of peptides that can be used in
CC   claimed immunostimulatory complexes of the invention that are
CC   specifically adapted to act as adjuvant and as peptide immunogen
CC   stabiliser. The complexes comprise a CpG oligonucleotide and a
CC   biologically active peptide immunogen. The complex is particulate and can
CC   efficiently present peptide immunogens to the cells of the immune system
CC   to produce an immune response. The complexes may be prepared with various
CC   ratios of peptides to CpG oligonucleotides to provide different physical
CC   properties, such as the size of the microparticle. An immunostimulatory
CC   complex comprising the present CD4 derived peptide can be used in an anti
CC   -CD4 immunotherapeutic vaccine for the treatment of HIV infection.
XX
SQ   Sequence 50 AA;

  Query Match             59.2%;  Score 90;  DB 7;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 11
ADD89953
ID   ADD89953 standard; protein; 65 AA.
XX
AC   ADD89953;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Foot-and-mouth disease peptide used in vaccine immunostimulant complex.
XX
KW   Immunostimulant; vaccine; immunogen; immunotherapy;
KW   foot-and-mouth disease.
XX
OS   Synthetic.
OS   Foot-and-mouth disease virus.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   20
FT                   /note= "Epsilon-lysine"
XX
PN   WO2003068169-A2.
XX
PD   21-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004711.
XX
PR   14-FEB-2002; 2002US-00076674.
PR   31-JAN-2003; 2003US-00076674.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Sokoll KK;
XX
DR   WPI; 2003-778890/73.
XX
PT   Stabilized immunostimulating complex, useful for vaccination, e.g.
PT   against human immune deficiency viruses, comprises cationic peptide
PT   immunogen and anionic oligonucleotide.
XX
PS   Claim 22; SEQ ID NO 13; 159pp; English.
XX
CC   The present sequence is that of a synthetic immunogenic peptide derived
CC   from foot-and-mouth disease (FMD) virus. This is an example of peptides
CC   that can be used in claimed immunostimulatory complexes of the invention
CC   that are specifically adapted to act as adjuvant and as peptide immunogen
CC   stabiliser. The complexes comprise a CpG oligonucleotide and a
CC   biologically active peptide immunogen. The complex is particulate and can
CC   efficiently present peptide immunogens to the cells of the immune system
CC   to produce an immune response. The complexes may be prepared with various
CC   ratios of peptides to CpG oligonucleotides to provide different physical
CC   properties, such as the size of the microparticle. An immunostimulatory
CC   complex comprising the present FMD virus derived peptide can be used in
CC   an anti-FMD vaccine for protective immunity against FMD.
XX
SQ   Sequence 65 AA;

  Query Match             57.2%;  Score 87;  DB 7;  Length 65;
  Best Local Similarity   94.7%;  Pred. No. 6.5e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              ||||||||||||:||||||
Db          1 ISITEIKGVIVHKIETILF 19


RESULT 12
ADD89952
ID   ADD89952 standard; protein; 65 AA.
XX
AC   ADD89952;
```

XX
DT 29-JAN-2004 (first entry)
XX
DE Foot-and-mouth disease peptide used in vaccine immunostimulant complex.
XX
KW Immunostimulant; vaccine; immunogen; immunotherapy;
KW foot-and-mouth disease.
XX
OS Synthetic.
OS Foot-and-mouth disease virus.
XX
FH Key Location/Qualifiers
FT Modified-site 20
FT /note= "Epsilon-lysine"
XX
PN WO2003068169-A2.
XX
PD 21-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-US004711.
XX
PR 14-FEB-2002; 2002US-00076674.
PR 31-JAN-2003; 2003US-00076674.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Sokoll KK;
XX
DR WPI; 2003-778890/73.
XX
PT Stabilized immunostimulating complex, useful for vaccination, e.g.
PT against human immune deficiency viruses, comprises cationic peptide
PT immunogen and anionic oligonucleotide.
XX
PS Claim 22; SEQ ID NO 12; 159pp; English.
XX
CC The present sequence is that of a synthetic immunogenic peptide derived
CC from foot-and-mouth disease (FMD) virus. This is an example of peptides
CC that can be used in claimed immunostimulatory complexes of the invention
CC that are specifically adapted to act as adjuvant and as peptide immunogen
CC stabiliser. The complexes comprise a CpG oligonucleotide and a
CC biologically active peptide immunogen. The complex is particulate and can
CC efficiently present peptide immunogens to the cells of the immune system
CC to produce an immune response. The complexes may be prepared with various
CC ratios of peptides to CpG oligonucleotides to provide different physical
CC properties, such as the size of the microparticle. An immunostimulatory
CC complex comprising the present FMD virus derived peptide can be used in
CC an anti-FMD vaccine for protective immunity against FMD.
XX
SQ Sequence 65 AA;

Query Match 54.6%; Score 83; DB 7; Length 65;
Best Local Similarity 89.5%; Pred. No. 2.8e-05;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy         12 ISITEIKGVIVHRIETILP 30
              |||:|||||||:||||||
Db          1 ISISEIKGVIVHKIETILP 19
```

RESULT 13
AAY91268
ID AAY91268 standard; peptide; 31 AA.
XX
AC AAY91268;
XX
DT 12-SEP-2003 (revised)
DT 22-MAY-2000 (first entry)
XX
DE Modified MVF Th epitope/HIV epitope, SEQ ID NO:146.
XX
KW Promiscuous T-cell epitope; measles virus F protein; MVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KW cholesteryl ester transport protein; anti-arteriosclerotic.
XX
OS Measles virus.
OS Human immunodeficiency virus 1.
OS Chimeric.
XX
PN WO9966957-A2.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US013975.
XX
PR 20-JUN-1998; 98US-00100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus.
XX
PS Claim 13; Page 63; 129pp; English.
XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and immunocastration)
CC ; for promoting the growth of animals; or for treating allergies or
CC arteriosclerosis. Incorporation of a promiscuous Th (functional in
CC genetically diverse subjects) into an immunogen improves capacity to
CC induce a strong T helper cell-mediated immune response, resulting in
CC production of antibodies against a target antigen. Th can replace carrier
CC proteins and pathogen-derived T helper epitopes. Sequence AAY91121
CC represents a promiscuous T helper epitope from the measles virus F (MVF)
CC protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246
CC represent synthetic Th epitopes based on the MVF Th epitope. Sequence
CC AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)
CC surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes
CC derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-
CC Y91244 are antigenic peptides comprising an LHRH sequence joined to a
CC promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide
CC used in these LHRH antigenic peptides. AAY91200 is somatostatin, and
CC AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th
CC epitope. Somatostatin immunogens may be used to promote growth in
CC livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and
CC AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may
CC be used to prevent HIV infection of T cells. AAY90212 is a modified
CC version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219
CC are Th epitope/IgE CH3 antigenic peptides which may be used in the
CC treatment of allergies. AAY91220 is a peptide derived from foot and mouth
CC disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this
CC peptide and a Th epitope. AAY91223 is a Plasmodium falciparum
CC circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS
CC antigen and an MVF Th epitope and may be used in a malaria vaccine.
CC AAY91228-Y91231 represent CETP-derived peptides and AAY91232-Y91241 are
CC immunogens comprising a CETP peptide and a Th epitope which may be used
CC to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247
CC and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-

CC Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and
CC HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1
CC vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory
CC invasin protein epitope from Yersinia species, and hinge spacer peptide,
CC both of which may optionally be used in the antigenic peptides of the
CC invention. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 31 AA;

Query Match 53.0%; Score 80.5; DB 3; Length 31;
Best Local Similarity 72.0%; Pred. No. 2.7e-05;
Matches 18; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 6 HDSGYKISITEIKGVIVHRIETILF 30
|:| : |||:|||||||:|| |||
Db 8 HES-WXISISEIKGVIVHKIEGILF 31

RESULT 14
AAY91260
ID AAY91260 standard; peptide; 29 AA.
XX
AC AAY91260;
XX
DT 12-SEP-2003 (revised)
DT 22-MAY-2000 (first entry)
XX
DE Modified MVF Th epitope/HIV epitope, SEQ ID NO:138.
XX
KW Promiscuous T-cell epitope; measles virus F protein; MVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KW cholesteryl ester transport protein; anti-arteriosclerotic.
XX
OS Measles virus.
OS Human immunodeficiency virus 1.
OS Chimeric.
XX
PN WO9966957-A2.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US013975.
XX
PR 20-JUN-1998; 98US-00100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus.
XX
PS Claim 13; Page 63; 129pp; English.
XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and immunocastration)
CC ; for promoting the growth of animals; or for treating allergies or
CC arteriosclerosis. Incorporation of a promiscuous Th (functional in
CC genetically diverse subjects) into an immunogen improves capacity to
CC induce a strong T helper cell-mediated immune response, resulting in
CC production of antibodies against a target antigen. Th can replace carrier
CC proteins and pathogen-derived T helper epitopes. Sequence AAY91121
CC represents a promiscuous T helper epitope from the measles virus F (MVF)
CC protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246
CC represent synthetic Th epitopes based on the MVF Th epitope. Sequence
CC AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)
CC surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes
CC derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-
CC Y91244 are antigenic peptides comprising an LHRH sequence joined to a
CC promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide
CC used in these LHRH antigenic peptides. AAY91200 is somatostatin, and
CC AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th
CC epitope. Somatostatin immunogens may be used to promote growth in
CC livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and
CC AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may
CC be used to prevent HIV infection of T cells. AAY90212 is a modified
CC version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219
CC are Th epitope/IgE CH3 antigenic peptides which may be used in the
CC treatment of allergies. AAY91220 is a peptide derived from foot and mouth
CC disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this
CC peptide and a Th epitope. AAY91223 is a Plasmodium falciparum
CC circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS
CC antigen and an MVF Th epitope and may be used in a malaria vaccine.
CC AAY91228-Y91231 represent CETP-derived peptides and AAY91232-Y91241 are
CC immunogens comprising a CETP peptide and a Th epitope which may be used
CC to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247
CC and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-
CC Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and
CC HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1
CC vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory
CC invasin protein epitope from Yersinia species, and hinge spacer peptide,
CC both of which may optionally be used in the antigenic peptides of the
CC invention. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 29 AA;

Query Match 51.3%; Score 78; DB 3; Length 29;
Best Local Similarity 77.3%; Pred. No. 6e-05;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 GYKISITEIKGVIVHRIETILF 30
| |||:|||||||:|| |||
Db 8 GPXISISEIKGVIVHKIEGILF 29

RESULT 15
AAY68551
ID AAY68551 standard; peptide; 19 AA.
XX
AC AAY68551;
XX
DT 05-MAY-2000 (first entry)
XX
DE Helper T cell epitope derived from SSAL Th1.
XX
KW Structured synthetic antigen library; SSAL; helper T cell epitope;
KW SSAL1 Th1; F protein; Measles virus; peptide immunogen; LHRH;
KW luteinising hormone-releasing hormone; spermatogenesis; ovulation;
KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;
KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.
XX
OS Synthetic.
OS Measles virus.
XX
PN WO9966952-A1.
XX
PD 29-DEC-1999.
XX

PF 21-JUN-1999; 99WO-US013960.
XX
PR 20-JUN-1998; 98US-00100414.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160562/14.
XX
PT New peptide immunogen containing luteinizing hormone-releasing hormone
PT antigen site and helper T cell epitope, for e.g. contraception and
PT treatment of cancer.
XX
PS Claim 1; Page 29; 102pp; English.
XX
CC The present sequence represents a helper T cell epitope derived from a
CC structured synthetic antigen library (SSAL) helper T cell epitope
CC designated SSAL1 Th1. SSAL Th1 is modelled after a promiscuous epitope
CC taken from the F protein of the Measles virus. The present epitope is
CC designed to be used in tandem with a target antigen, luteinising hormone-
CC releasing hormone (LHRH). The epitope is used to construct peptide
CC immunogens of the invention, which contain at least one antigenic target
CC site, i.e. luteinising hormone-releasing hormone (LHRH) or its analogue,
CC and an artificial helper T cell epitope (Th). The peptide immunogens
CC cause induction of a specific immune response to LHRH which is involved
CC in regulation of spermatogenesis, ovulation, oestrus, sexual development
CC and secretion of sex hormones. Provision of a promiscuous T helper
CC epitope (which is functional in genetically diverse subjects) provides
CC optimum immunogenicity to the B cell epitopes of the target antigen and
CC thus high antibody titres against the target antigen. The peptide
CC immunogens of the invention are used to vaccinate against mammalian LHRH,
CC for use as (reversible) contraceptive; control of hormone-dependent
CC tumours (cancer of prostate or breast, also endometriosis); to prevent
CC boar taint (and improve meat quality) and for immunocastration
XX
SQ Sequence 19 AA;

Query Match 50.0%; Score 76; DB 3; Length 19;
Best Local Similarity 84.2%; Pred. No. 7.2e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy         12 ISITEIKGVIVHRIETILF 30
              |||:||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19
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Search completed: June 18, 2004, 19:58:51
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GenCore version 5.1.6

OM protein - protein search, using sw model

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(without alignments)
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Perfect score: 152
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	76	50.0	19	3	US-09-100-414B-15	Sequence 15, Appl
2	76	50.0	19	3	US-09-303-323-15	Sequence 15, Appl
3	76	50.0	19	4	US-09-770-014-15	Sequence 15, Appl
4	76	50.0	31	3	US-09-100-414B-53	Sequence 53, Appl
5	76	50.0	31	3	US-09-303-323-53	Sequence 53, Appl
6	76	50.0	31	4	US-09-770-014-53	Sequence 53, Appl
7	76	50.0	35	3	US-09-100-414B-80	Sequence 80, Appl
8	76	50.0	35	3	US-09-303-323-80	Sequence 80, Appl
9	76	50.0	35	4	US-09-770-014-80	Sequence 80, Appl
10	76	50.0	46	3	US-09-100-414B-96	Sequence 96, Appl
11	76	50.0	46	3	US-09-303-323-96	Sequence 96, Appl
12	76	50.0	46	4	US-09-770-014-96	Sequence 96, Appl
13	76	50.0	47	3	US-09-100-414B-60	Sequence 60, Appl
14	76	50.0	47	3	US-09-303-323-60	Sequence 60, Appl
15	76	50.0	47	4	US-09-770-014-60	Sequence 60, Appl
16	76	50.0	49	3	US-09-100-414B-57	Sequence 57, Appl
17	76	50.0	49	3	US-09-303-323-57	Sequence 57, Appl
18	76	50.0	49	4	US-09-770-014-57	Sequence 57, Appl
19	76	50.0	80	3	US-09-100-600A-30	Sequence 30, Appl
20	71	46.7	19	3	US-09-100-414B-17	Sequence 17, Appl
21	71	46.7	19	3	US-09-303-323-17	Sequence 17, Appl
22	71	46.7	19	4	US-09-770-014-17	Sequence 17, Appl
23	71	46.7	31	3	US-09-100-414B-55	Sequence 55, Appl
24	71	46.7	31	3	US-09-303-323-55	Sequence 55, Appl
25	71	46.7	31	4	US-09-770-014-55	Sequence 55, Appl
26	69	45.4	19	3	US-09-100-414B-18	Sequence 18, Appl
27	69	45.4	19	3	US-09-100-414B-19	Sequence 19, Appl
28	69	45.4	19	3	US-09-100-414B-20	Sequence 20, Appl
29	69	45.4	19	3	US-09-303-323-18	Sequence 18, Appl
30	69	45.4	19	3	US-09-303-323-19	Sequence 19, Appl
31	69	45.4	19	3	US-09-303-323-20	Sequence 20, Appl
32	69	45.4	19	4	US-09-770-014-18	Sequence 18, Appl
33	69	45.4	19	4	US-09-770-014-19	Sequence 19, Appl
34	69	45.4	19	4	US-09-770-014-20	Sequence 20, Appl
35	69	45.4	31	3	US-09-100-414B-56	Sequence 56, Appl
36	69	45.4	31	3	US-09-100-414B-59	Sequence 59, Appl
37	69	45.4	31	3	US-09-100-414B-61	Sequence 61, Appl
38	69	45.4	31	3	US-09-303-323-56	Sequence 56, Appl
39	69	45.4	31	3	US-09-303-323-59	Sequence 59, Appl
40	69	45.4	31	3	US-09-303-323-61	Sequence 61, Appl
41	69	45.4	31	4	US-09-770-014-56	Sequence 56, Appl
42	69	45.4	31	4	US-09-770-014-59	Sequence 59, Appl
43	69	45.4	31	4	US-09-770-014-61	Sequence 61, Appl
44	69	45.4	35	3	US-09-100-414B-81	Sequence 81, Appl
45	69	45.4	35	3	US-09-303-323-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-09-100-414B-15
; Sequence 15, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-15

Query Match 50.0%; Score 76; DB 3; Length 19;
Best Local Similarity 84.2%; Pred. No. 9.1e-06;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy         12 ISITEIKGVIVHRIETILF 30
              |||:|||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19
```

RESULT 2

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US-09-303-323-15
; Sequence 15, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/303,323
;      FILING DATE:  30-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-303-323-15

  Query Match             50.0%;  Score 76;  DB 3;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 9.1e-06;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILP 30
              |||:||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILP 19


RESULT 3
US-09-770-014-15
; Sequence 15, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/770,014
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-15

  Query Match             50.0%;  Score 76;  DB 4;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 9.1e-06;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILP 30
              |||:||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILP 19


RESULT 4
US-09-100-414B-53
; Sequence 53, Application US/09100414B
; Patent No. 6025468
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/100,414B
;      FILING DATE:  20-JUNE-1998
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-100-414B-53

  Query Match             50.0%;  Score 76;  DB 3;  Length 31;
  Best Local Similarity   84.2%;  Pred. No. 1.7e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;
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```
Qy          12 ISITEIKGVIVHRIETILF 30
               |||:|||||||||:|| |||
Db           1 ISISEIKGVIVHKIEGILF 19


RESULT 5
US-09-303-323-53
; Sequence 53, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/303,323
;      FILING DATE:  30-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-303-323-53

  Query Match             50.0%;  Score 76;  DB 3;  Length 31;
  Best Local Similarity   84.2%;  Pred. No. 1.7e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 ISITEIKGVIVHRIETILF 30
               |||:|||||||||:|| |||
Db           1 ISISEIKGVIVHKIEGILF 19


RESULT 6
US-09-770-014-53
; Sequence 53, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/770,014
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-53

  Query Match             50.0%;  Score 76;  DB 4;  Length 31;
  Best Local Similarity   84.2%;  Pred. No. 1.7e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 ISITEIKGVIVHRIETILF 30
               |||:|||||||||:|| |||
Db           1 ISISEIKGVIVHKIEGILF 19


RESULT 7
US-09-100-414B-80
; Sequence 80, Application US/09100414B
; Patent No. 6025468
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/100,414B
;      FILING DATE:  20-JUNE-1998
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  80:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-100-414B-80

  Query Match             50.0%;  Score 76;  DB 3;  Length 35;
  Best Local Similarity   84.2%;  Pred. No. 2e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||:|||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 8
US-09-303-323-80
; Sequence 80, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/303,323
;      FILING DATE:  30-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  80:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-303-323-80

  Query Match             50.0%;  Score 76;  DB 3;  Length 35;
  Best Local Similarity   84.2%;  Pred. No. 2e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||:|||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 9
US-09-770-014-80
; Sequence 80, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/770,014
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  80:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-80

  Query Match             50.0%;  Score 76;  DB 4;  Length 35;
  Best Local Similarity   84.2%;  Pred. No. 2e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||:|||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 10
US-09-100-414B-96
; Sequence 96, Application US/09100414B
; Patent No. 6025468
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/100,414B
;      FILING DATE:  20-JUNE-1998
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  96:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  46 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-100-414B-96

  Query Match           50.0%;  Score 76;  DB 3;  Length 46;
  Best Local Similarity  84.2%;  Pred. No. 2.8e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||:|||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 11
US-09-303-323-96
; Sequence 96, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/303,323
;      FILING DATE:  30-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  96:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  46 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-303-323-96

  Query Match           50.0%;  Score 76;  DB 3;  Length 46;
  Best Local Similarity  84.2%;  Pred. No. 2.8e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||:|||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 12
US-09-770-014-96
; Sequence 96, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/770,014
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  96:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  46 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-96

  Query Match           50.0%;  Score 76;  DB 4;  Length 46;
  Best Local Similarity  84.2%;  Pred. No. 2.8e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||:|||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 13
US-09-100-414B-60
; Sequence 60, Application US/09100414B
; Patent No. 6025468
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
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```
;      APPLICATION NUMBER:  US/09/100,414B
;      FILING DATE:  20-JUNE-1998
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  47 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-100-414B-60

  Query Match             50.0%;  Score 76;  DB 3;  Length 47;
  Best Local Similarity   84.2%;  Pred. No. 2.8e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||:|||||||||:|| |||
Db         17 ISISEIKGVIVHKIEGILF 35


RESULT 14
US-09-303-323-60
; Sequence 60, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/303,323
;      FILING DATE:  30-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  47 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-303-323-60

  Query Match             50.0%;  Score 76;  DB 3;  Length 47;
  Best Local Similarity   84.2%;  Pred. No. 2.8e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||:|||||||||:|| |||
Db         17 ISISEIKGVIVHKIEGILF 35


RESULT 15
US-09-770-014-60
; Sequence 60, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/770,014
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  47 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-60

  Query Match             50.0%;  Score 76;  DB 4;  Length 47;
  Best Local Similarity   84.2%;  Pred. No. 2.8e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||:|||||||||:|| |||
Db         17 ISISEIKGVIVHKIEGILF 35


Search completed: June 18, 2004, 20:04:45
Job time : 11.7791 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 20:02:36 ; Search time 33.865 Seconds
(without alignments)
250.093 Million cell updates/sec

Title: US-09-865-294A-71
Perfect score: 152
Sequence: 1 DAEFRHDSGYKISITEIKGVIVHRIETILF 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	152	100.0	30	10	US-09-865-294-71	Sequence 71, Appl
2	141	92.8	32	10	US-09-865-294-72	Sequence 72, Appl
3	140	92.1	34	10	US-09-865-294-73	Sequence 73, Appl
4	133	87.5	48	10	US-09-865-294-74	Sequence 74, Appl
5	126	82.9	34	10	US-09-865-294-75	Sequence 75, Appl
6	119	78.3	34	10	US-09-865-294-76	Sequence 76, Appl
7	90	59.2	19	10	US-09-865-294-51	Sequence 51, Appl
8	90	59.2	31	14	US-10-076-674-6	Sequence 6, Appli
9	90	59.2	31	15	US-10-355-161A-6	Sequence 6, Appli
10	90	59.2	45	14	US-10-076-674-11	Sequence 11, Appl
11	90	59.2	45	15	US-10-355-161A-11	Sequence 11, Appl
12	90	59.2	50	14	US-10-076-674-4	Sequence 4, Appli
13	90	59.2	50	15	US-10-355-161A-4	Sequence 4, Appli
14	87	57.2	65	15	US-10-355-161A-13	Sequence 13, Appl
15	83	54.6	65	15	US-10-355-161A-12	Sequence 12, Appl
16	76	50.0	19	10	US-09-747-802-49	Sequence 49, Appl
17	76	50.0	19	10	US-09-747-802-55	Sequence 55, Appl
18	76	50.0	19	10	US-09-865-294-38	Sequence 38, Appl
19	76	50.0	19	10	US-09-865-294-41	Sequence 41, Appl
20	76	50.0	19	10	US-09-865-294-47	Sequence 47, Appl
21	76	50.0	30	10	US-09-747-802-80	Sequence 80, Appl
22	76	50.0	32	10	US-09-747-802-82	Sequence 82, Appl
23	76	50.0	34	10	US-09-747-802-78	Sequence 78, Appl
24	76	50.0	39	10	US-09-747-802-84	Sequence 84, Appl
25	76	50.0	46	10	US-09-747-802-74	Sequence 74, Appl
26	76	50.0	46	10	US-09-747-802-76	Sequence 76, Appl
27	71	46.7	19	10	US-09-747-802-48	Sequence 48, Appl
28	71	46.7	19	10	US-09-865-294-40	Sequence 40, Appl
29	69	45.4	19	10	US-09-747-802-46	Sequence 46, Appl
30	69	45.4	19	10	US-09-747-802-50	Sequence 50, Appl
31	69	45.4	19	10	US-09-747-802-51	Sequence 51, Appl
32	69	45.4	19	10	US-09-747-802-54	Sequence 54, Appl
33	69	45.4	19	10	US-09-747-802-56	Sequence 56, Appl
34	69	45.4	19	10	US-09-865-294-42	Sequence 42, Appl
35	69	45.4	19	10	US-09-865-294-43	Sequence 43, Appl
36	69	45.4	19	10	US-09-865-294-46	Sequence 46, Appl
37	69	45.4	19	10	US-09-865-294-48	Sequence 48, Appl
38	69	45.4	30	10	US-09-747-802-81	Sequence 81, Appl
39	69	45.4	32	10	US-09-747-802-83	Sequence 83, Appl
40	69	45.4	34	10	US-09-747-802-79	Sequence 79, Appl
41	69	45.4	39	10	US-09-747-802-85	Sequence 85, Appl
42	69	45.4	46	10	US-09-747-802-75	Sequence 75, Appl
43	69	45.4	46	10	US-09-747-802-77	Sequence 77, Appl
44	64.5	42.4	35	9	US-09-972-475-15	Sequence 15, Appl
45	64.5	42.4	35	15	US-10-463-729-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-865-294-71
; Sequence 71, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Measles virus
US-09-865-294-71

Query Match 100.0%; Score 152; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.6e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYKISITEIKGVIVHRIETILF 30
||||||||||||||||||||||||||||||
Db 1 DAEFRHDSGYKISITEIKGVIVHRIETILF 30

RESULT 2
US-09-865-294-72
; Sequence 72, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294

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;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
;    LENGTH: 32
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-72

  Query Match             92.8%;  Score 141;  DB 10;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 9e-15;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGY--KISITEIKGVIVHRIETILF 30
              ||||||||||  ||||||||||||||||||||
Db          1 DAEFRHDSGYEVKISITEIKGVIVHRIETILF 32


RESULT 3
US-09-865-294-73
; Sequence 73, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
;    LENGTH: 34
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-73

  Query Match             92.1%;  Score 140;  DB 10;  Length 34;
  Best Local Similarity   88.2%;  Pred. No. 1.4e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    4;  Gaps    1;

Qy          1 DAEFRHDSGY----KISITEIKGVIVHRIETILF 30
              ||||||||||    ||||||||||||||||||||
Db          1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34


RESULT 4
US-09-865-294-74
; Sequence 74, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
;    LENGTH: 48
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-74

  Query Match             87.5%;  Score 133;  DB 10;  Length 48;
  Best Local Similarity   62.5%;  Pred. No. 2.6e-13;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels   18;  Gaps    1;

Qy          1 DAEFRHDSGY-----------------KISITEIKGVIVHRIETILF 30
              ||||||||||                 ||||||||||||||||||||
Db          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48


RESULT 5
US-09-865-294-75
; Sequence 75, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
;    LENGTH: 34
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-75

  Query Match             82.9%;  Score 126;  DB 10;  Length 34;
  Best Local Similarity   79.4%;  Pred. No. 2.1e-12;
  Matches   27;  Conservative    2;  Mismatches    1;  Indels    4;  Gaps    1;

Qy          1 DAEFRHDSGY----KISITEIKGVIVHRIETILF 30
              ||||||||||    ||||:|||||||:|| |||
Db          1 DAEFRHDSGYEVHHKISISEIKGVIVHKIEGILF 34


RESULT 6
US-09-865-294-76
; Sequence 76, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
;    LENGTH: 34
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-76

  Query Match             78.3%;  Score 119;  DB 10;  Length 34;
  Best Local Similarity   79.4%;  Pred. No. 2.7e-11;
  Matches   27;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy          1 DAEFRHDSGY----KISITEIKGVIVHRIETILF 30
              ||||||||||    |||||||: ||| |||||||
Db          1 DAEFRHDSGYEVHHKISITEIRTVIVTRIETILF 34


RESULT 7
US-09-865-294-51
; Sequence 51, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
;    LENGTH: 19
;    TYPE: PRT
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;   ORGANISM: Measles virus
US-09-865-294-51

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  Best Local Similarity   100.0%;  Pred. No. 4.5e-07;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 8
US-10-076-674-6
; Sequence 6, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/076,674
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-6

  Query Match             59.2%;  Score 90;  DB 14;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 8e-07;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 9
US-10-355-161A-6
; Sequence 6, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-6

  Query Match             59.2%;  Score 90;  DB 15;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 8e-07;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 10
US-10-076-674-11
; Sequence 11, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/076,674
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 45
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-11

  Query Match             59.2%;  Score 90;  DB 14;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 11
US-10-355-161A-11
; Sequence 11, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 45
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-11

  Query Match             59.2%;  Score 90;  DB 15;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 12
US-10-076-674-4
; Sequence 4, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
```

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;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/076,674
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 50
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-4

  Query Match             59.2%;  Score 90;  DB 14;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              ||||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 13
US-10-355-161A-4
; Sequence 4, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 50
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-4

  Query Match             59.2%;  Score 90;  DB 15;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              ||||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 14
US-10-355-161A-13
; Sequence 13, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
;   LENGTH: 65
;   TYPE: PRT
;   ORGANISM: Foot-and-mouth disease virus
US-10-355-161A-13

  Query Match             57.2%;  Score 87;  DB 15;  Length 65;
  Best Local Similarity   94.7%;  Pred. No. 5.8e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              ||||||||||||:||||||
Db          1 ISITEIKGVIVHKIETILF 19


RESULT 15
US-10-355-161A-12
; Sequence 12, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 65
;   TYPE: PRT
;   ORGANISM: Foot-and-mouth disease virus
US-10-355-161A-12

  Query Match             54.6%;  Score 83;  DB 15;  Length 65;
  Best Local Similarity   89.5%;  Pred. No. 2.4e-05;
  Matches   17;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 ISITEIKGVIVHRIETILF 30
              |||:||||||||:||||||
Db          1 ISISEIKGVIVHKIETILF 19


Search completed: June 18, 2004, 20:23:46
Job time : 33.865 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:45 ; Search time 9.0184 Seconds
(without alignments)
319.984 Million cell updates/sec

Title: US-09-865-294A-71
Perfect score: 152
Sequence: 1 DAEFRHDSGYKISITEIKGVIVHRIETILF 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	64	42.1	546	1	VGNZRL	cell fusion glycop
2	62	40.8	42	2	PN0512	beta-amyloid prote
3	62	40.8	57	2	B60045	Alzheimer's diseas
4	62	40.8	57	2	F60045	Alzheimer's diseas
5	62	40.8	57	2	G60045	Alzheimer's diseas
6	62	40.8	57	2	D60045	Alzheimer's diseas
7	62	40.8	57	2	A60045	Alzheimer's diseas
8	62	40.8	57	2	B60045	Alzheimer's diseas
9	62	40.8	82	2	PQ0438	Alzheimer's diseas
10	62	40.8	695	1	A49795	Alzheimer's diseas
11	62	40.8	770	1	QRHUA4	Alzheimer's diseas
12	61	40.1	546	2	S47300	gene F protein - r
13	60	39.5	546	1	VGNZRK	cell fusion glycop
14	60	39.5	546	2	S55386	cell fusion protei
15	60	39.5	546	2	S47305	gene F protein - r
16	59.5	39.1	552	2	S47034	cell fusion protei
17	59	38.8	542	2	JQ2223	cell fusion protei
18	59	38.8	662	1	VGNZCD	cell fusion glycop
19	59	38.8	662	2	S21382	cell fusion protei
20	58	38.2	282	2	PQ0376	cell fusion glycop
21	58	38.2	282	2	PQ0388	cell fusion glycop
22	58	38.2	534	1	JU0274	cell fusion glycop
23	58	38.2	550	1	B48556	cell fusion glycop
24	58	38.2	553	1	VGNZMV	cell fusion glycop
25	58	38.2	631	1	VGNZPD	cell fusion glycop
26	58	38.2	631	1	A48346	cell fusion glycop
27	53	34.9	229	2	P86180	hypothetical prote
28	52	34.2	220	2	T00801	probable synaptobr
29	52	34.2	240	2	T47589	synaptobrevin-like
30	51	33.6	236	2	A90190	hypothetical prote
31	51	33.6	421	2	T33811	hypothetical prote
32	51	33.6	695	2	A27485	Alzheimer's diseas
33	51	33.6	695	2	S00550	Alzheimer's diseas
34	50	32.9	33	2	S23094	beta-amyloid prote
35	50	32.9	649	2	B38129	bo-type ubiquinol
36	49.5	32.6	219	2	D89923	endonuclease-like
37	49	32.2	112	2	S26221	cruciferin (clone
38	49	32.2	458	2	E83588	RNA helicase DbpA
39	48.5	31.9	356	2	D96537	hypothetical prote
40	48.5	31.9	426	2	S76247	hypothetical prote
41	48.5	31.9	792	2	B71539	probable omp85 ana
42	48.5	31.9	792	2	H81693	outer membrane pro
43	48	31.6	175	2	D86180	hypothetical prote
44	48	31.6	221	2	F84741	probable synaptobr
45	48	31.6	497	2	A82545	two-component syst

ALIGNMENTS

RESULT 1
VGNZRL
cell fusion glycoprotein precursor - rinderpest virus (strain L)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: rinderpest virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Accession: A28921
R;Tsukiyama, K.; Yoshikawa, Y.; Yamanouchi, K.
Virology 164, 523-530, 1988
A;Title: Fusion glycoprotein (F) of rinderpest virus: entire nucleotide sequence of the
A;Reference number: A28921; MUID:88219541; PMID:3285575
A;Accession: A28921
A;Molecule type: mRNA
A;Residues: 1-546 <TSU>
A;Cross-references: GB:M20870; NID:g333898; PIDN:AAA47399.1; PID:g333899
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-104/Product: cell fusion glycoprotein F2 #status predicted <FG2>
F;105-546/Product: cell fusion glycoprotein F1 #status predicted <FG1>
F;109-133/Domain: transmembrane #status predicted <TN1>
F;485-513/Domain: transmembrane #status predicted <TN2>
F;25,57,63/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 42.1%; Score 64; DB 1; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.18;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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Qy         13 SITEIKGVIVHRIETILF 30
              |::|||||||||:|:: :
Db        283 SLSEIKGVIVHRLESVSY 300
```

RESULT 2
PN0512
beta-amyloid protein - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PN0512
R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragme
A;Reference number: PN0512; MUID:93290653; PMID:7685598
A;Accession: PN0512
A;Molecule type: protein
A;Residues: 1-42 <SHI>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; amyloid

Query Match 40.8%; Score 62; DB 2; Length 42;

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  Best Local Similarity   40.6%;  Pred. No. 0.022;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 32


RESULT 3
E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C;Species: Ovis sp. (sheep)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: E60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: E60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56130
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match             40.8%;  Score 62;  DB 2;  Length 57;
  Best Local Similarity   40.6%;  Pred. No. 0.03;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db          6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 37


RESULT 4
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: F60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: F60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match             40.8%;  Score 62;  DB 2;  Length 57;
  Best Local Similarity   40.6%;  Pred. No. 0.03;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db          6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 37


RESULT 5
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: G60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: G60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56126
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match             40.8%;  Score 62;  DB 2;  Length 57;
  Best Local Similarity   40.6%;  Pred. No. 0.03;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db          6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 37


RESULT 6
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: D60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: D60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56124
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match             40.8%;  Score 62;  DB 2;  Length 57;
  Best Local Similarity   40.6%;  Pred. No. 0.03;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db          6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 37


RESULT 7
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: A60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: A60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56125
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match             40.8%;  Score 62;  DB 2;  Length 57;
  Best Local Similarity   40.6%;  Pred. No. 0.03;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db          6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 37


RESULT 8
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C;Species: Ursus maritimus (polar bear)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: B60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
```

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A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: B60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match             40.8%;  Score 62;  DB 2;  Length 57;
  Best Local Similarity   40.6%;  Pred. No. 0.03;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db          6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 37


RESULT 9
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: PQ0438; C60045
R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A;Reference number: PQ0438; MUID:93075180; PMID:1445331
A;Accession: PQ0438
A;Molecule type: DNA
A;Residues: 1-82 <DAV>
A;Cross-references: GB:M83558; GB:M83657
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: C60045
A;Molecule type: mRNA
A;Residues: 12-68 <JOH>
A;Cross-references: EMBL:X56129
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

  Query Match             40.8%;  Score 62;  DB 2;  Length 82;
  Best Local Similarity   40.6%;  Pred. No. 0.045;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db         17 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 48


RESULT 10
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49795
R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a p
A;Reference number: A49795; MUID:91273117; PMID:1905108
A;Accession: A49795
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-695 <POD>
A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing

  Query Match             40.8%;  Score 62;  DB 1;  Length 695;
  Best Local Similarity   40.6%;  Pred. No. 0.46;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 628


RESULT 11
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibi
N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44
4668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S3
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288,'V',365-770 <LEM1>
A;Cross-references: EMBL:X13466
A;Note: alternative splice form APP(695)
R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A;Note: alternative splice form APP(695)
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A;Reference number: A32277; MUID:89165870; PMID:2538123
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAF>
A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A;Reference number: A33260; MUID:89392030; PMID:2675837
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMB
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMB
A;Molecule type: DNA
A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
```

A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheime
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 689-716,'F',718-737 <MUR>
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692,'G',694-718 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288,'V',365-770 <KAN>
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756,'S',758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muell
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pre
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.P.; Nev
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associa
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344,'I',365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; D
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344,'I',365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibito
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashto
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288,'V',365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 60
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 6
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K

Query Match 40.8%; Score 62; DB 1; Length 770;
Best Local Similarity 40.6%; Pred. No. 0.51;
Matches 13; Conservative 4; Mismatches 5; Indels 10; Gaps 1;

Qy 1 DAEFRHDSGYKI----------SITEIKGVIV 22

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Db        672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 703


RESULT 12
S47300
gene F protein - rinderpest virus
C;Species: rinderpest virus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Oct-1999
C;Accession: S47300; PQ0865
R;Evans, S.A.; Baron, M.D.; Chamberlain, R.W.; Goatley, L.; Barrett, T.
submitted to the EMBL Data Library, March 1994
A;Description: The complete nucleotide sequence of the fusion protein gene of the vaccin
A;Reference number: S47299
A;Accession: S47300
A;Molecule type: DNA
A;Residues: 1-546 <EVA>
A;Cross-references: EMBL:Z31656; NID:g535406; PIDN:CAA83482.1; PID:g535407
R;Chamberlain, R.W.; Wamwayi, H.M.; Hockley, E.; Shaila, M.S.; Goatley, L.; Knowles, N.J
J. Gen. Virol. 74, 2775-2780, 1993
A;Title: Evidence for different lineages of rinderpest virus reflecting their geographic
A;Reference number: PQ0865; MUID:94103786; PMID:8277286
A;Accession: PQ0865
A;Molecule type: mRNA
A;Residues: 86-191 <CHA>
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein

  Query Match             40.1%;  Score 61;  DB 2;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 0.5;
  Matches   11;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 SITEIKGVIVHRIETILF 30
              |::|||||||||:| : :
Db        283 SLSEIKGVIVHRLEGVSY 300


RESULT 13
VGNZRK
cell fusion glycoprotein precursor - rinderpest virus (strain Kabete O)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: rinderpest virus
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 25-Oct-1996
C;Accession: A31051
R;Hsu, D.; Yamanaka, M.; Miller, J.; Dale, B.; Grubman, M.; Yilma, T.
Virology 166, 149-153, 1988
A;Title: Cloning of the fusion gene of rinderpest virus: comparative sequence analysis w
A;Reference number: A31051; MUID:88322864; PMID:3413983
A;Accession: A31051
A;Molecule type: genomic RNA
A;Residues: 1-546 <HSU>
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-108/Product: cell fusion glycoprotein F2 #status predicted <FF1>
F;109-546/Product: cell fusion glycoprotein F1 #status predicted <FF2>
F;109-134/Domain: transmembrane #status predicted <TN1>
F;491-513/Domain: transmembrane #status predicted <TN2>
F;25,57,63,518/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             39.5%;  Score 60;  DB 1;  Length 546;
  Best Local Similarity   55.6%;  Pred. No. 0.7;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 SITEIKGVIVHRIETILF 30
              |::||||||:||:| : :
Db        283 SLSEIKGVIIHRLEGVSY 300


RESULT 14
S55386
cell fusion protein - peste-des-petits-ruminants virus (strain 75/1)
N;Alternate names: F protein
C;Species: peste-des-petits-ruminants virus
A;Variety: strain 75/1
C;Date: 23-May-1997 #sequence_revision 23-May-1997 #text_change 20-Sep-1999
C;Accession: S55386
R;Meyer, G.; Diallo, A.
submitted to the EMBL Data Library, September 1994
A;Description: The nucleotide sequence of fusion protein gene of the Peste des petits ru
to each virus.
A;Reference number: S55386
A;Accession: S55386
A;Molecule type: DNA
A;Residues: 1-546 <MEY>
A;Cross-references: EMBL:Z37017; NID:g854372; PIDN:CAA85451.1; PID:g854373
A;Experimental source: strain 75/1; cell line vero
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: membrane fusion

  Query Match             39.5%;  Score 60;  DB 2;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 0.7;
  Matches   11;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 SITEIKGVIVHRIETILF 30
              :::|||||||:|| | :
Db        283 TLSEIKGVIVHKIEAISY 300


RESULT 15
S47305
gene F protein - rinderpest virus
C;Species: rinderpest virus
C;Date: 20-Oct-1994 #sequence_revision 08-Sep-1995 #text_change 20-Sep-1999
C;Accession: S47305; S47301
R;Baron, M.D.; Barrett, T.
submitted to the EMBL Data Library, March 1994
A;Description: The sequence of the N and L genes of Rinderpest virus, and the 5O and 3O
A;Reference number: S47283
A;Accession: S47305
A;Molecule type: mRNA
A;Residues: 1-546 <BAR>
A;Cross-references: EMBL:Z30697; NID:g535396; PIDN:CAA83181.1; PID:g535401; EMBL:Z30700;
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: transmembrane protein

  Query Match             39.5%;  Score 60;  DB 2;  Length 546;
  Best Local Similarity   55.6%;  Pred. No. 0.7;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 SITEIKGVIVHRIETILF 30
              |::||||||:||:| : :
Db        283 SLSEIKGVIIHRLEGVSY 300


Search completed: June 18, 2004, 20:03:30
Job time : 10.0184 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:55 ; Search time 5.88957 Seconds
(without alignments)
265.232 Million cell updates/sec

Title: US-09-865-294A-71
Perfect score: 152
Sequence: 1 DAEFRHDSGYKISITEIKGVIVHRIETILF 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	64	42.1	546	1	VGLF_RINDL	P10864 rinderpest
2	62	40.8	57	1	A4_URSMA	Q29149 ursus marit
3	62	40.8	58	1	A4_CANFA	Q28280 canis famil
4	62	40.8	58	1	A4_RABIT	Q28748 oryctolagus
5	62	40.8	58	1	A4_SHEEP	Q28757 ovis aries
6	62	40.8	59	1	A4_BOVIN	Q28053 bos taurus
7	62	40.8	751	1	A4_SAISC	Q95241 s amyloid b
8	62	40.8	770	1	A4_CAVPO	Q60495 c amyloid b
9	62	40.8	770	1	A4_HUMAN	P05067 h amyloid b
10	62	40.8	770	1	A4_MACFA	P53601 m amyloid b
11	62	40.8	770	1	A4_PIG	P79307 s amyloid b
12	61	40.1	546	1	VGLF_RINDB	P41360 rinderpest
13	60	39.5	546	1	VGLF_RINDR	P41356 rinderpest
14	59	38.8	662	1	VGLF_CDVO	P12569 canine dist
15	58	38.2	534	1	VGLF_MEASY	P26032 measles vir
16	58	38.2	550	1	VGLF_MEASA	P35973 measles vir
17	58	38.2	550	1	VGLF_MEASE	P08300 measles vir
18	58	38.2	631	1	VGLF_PHODV	P28886 phocine dis
19	54	35.5	546	1	VGLF_RINDK	P12574 rinderpest
20	53	34.9	229	1	V726_ARATH	Q9mas5 arabidopsis
21	52	34.2	220	1	V725_ARATH	O48850 arabidopsis
22	52	34.2	240	1	V727_ARATH	Q9m376 arabidopsis
23	51	33.6	235	1	PUR7_THETN	Q8rc58 thermoanaer
24	51	33.6	770	1	A4_MOUSE	P12023 m amyloid b
25	51	33.6	770	1	A4_RAT	P08592 r amyloid b
26	50	32.9	529	1	VGLF_MEASI	P26031 measles vir
27	50	32.9	649	1	QOX1_BACSU	P34956 bacillus su
28	48.5	31.9	356	1	BCA6_ARATH	Q9lpm9 arabidopsis
29	48	31.6	219	1	V721_ARATH	Q9ztw3 arabidopsis
30	48	31.6	221	1	V722_ARATH	P47192 arabidopsis
31	47.5	31.2	409	1	NQO4_THETH	Q56220 thermus the
32	47.5	31.2	625	1	T9S4_HUMAN	Q92544 homo sapien
33	47	30.9	264	1	DAPB_BACHD	Q9kc93 bacillus ha
34	47	30.9	571	1	DCP1_SCHPO	Q09737 schizosacch
35	45	29.6	247	1	CAH_METTE	P40881 methanosarc
36	45	29.6	397	1	AAT_STRVG	Q60013 streptomyce
37	45	29.6	488	1	CRUA_BRANA	P11090 brassica na
38	45	29.6	490	1	CRU1_BRANA	P33523 brassica na
39	45	29.6	496	1	CRU2_BRANA	P33524 brassica na
40	45	29.6	680	1	OPDA_ECOLI	P27298 escherichia
41	45	29.6	1005	1	MANA_DICDI	P34098 dictyosteli
42	44.5	29.3	139	1	Y024_METJA	Q60334 methanococc
43	44.5	29.3	282	1	IF34_SCHPO	P78795 schizosacch
44	44.5	29.3	670	1	PBP_STAAU	P07944 staphylococ
45	44	28.9	260	1	YG38_METJA	Q59032 methanococc

ALIGNMENTS

RESULT 1
VGLF_RINDL
ID VGLF_RINDL STANDARD; PRT; 546 AA.
AC P10864;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Rinderpest virus (strain L) (RDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11243;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219541; PubMed=3285575;
RA Tsukiyama K., Yoshikawa Y., Yamanouchi K.;
RT "Fusion glycoprotein (F) of rinderpest virus: entire nucleotide
RT sequence of the F mRNA, and several features of the F protein.";
RL Virology 164:523-530(1988).
CC -!- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC --

CC --
DR EMBL; M20870; AAA47399.1; -.
DR PIR; A28921; VGNZRL.
DR HSSP; P04849; 1SVF.
DR InterPro; IPR000776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 546 FUSION GLYCOPROTEIN F0.
FT CHAIN 20 108 F2 PROTEIN.
FT CHAIN 109 546 F1 PROTEIN.
FT DOMAIN 104 108 ARG/LYS-RICH (BASIC).
FT TRANSMEM 109 133 POTENTIAL.
FT TRANSMEM 484 513 POTENTIAL.
FT DOMAIN 514 517 ARG/LYS-RICH (BASIC).
FT DISULFID 64 191 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 546 AA; 58911 MW; 985029418F28FPB5 CRC64;

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  Query Match             42.1%;  Score 64;  DB 1;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 0.067;
  Matches   11;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 SITEIKGVIVHRIETILF 30
              |::|||||||||:|:: :
Db        283 SLSEIKGVIVHRLESVSY 300


RESULT 2
A4_URSMA
ID   A4_URSMA       STANDARD;      PRT;    57 AA.
AC   Q29149;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Ursus maritimus (Polar bear) (Thalarctos maritimus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX   NCBI_TaxID=29073;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56128; CAA39593.1; -.
DR   PIR; B60045; B60045.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   NON_TER      57     57
SQ   SEQUENCE   57 AA;  6172 MW;  84209D88EBA82DFA CRC64;

  Query Match             40.8%;  Score 62;  DB 1;  Length 57;
  Best Local Similarity   40.6%;  Pred. No. 0.012;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db          6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 37


RESULT 3
A4_CANFA
ID   A4_CANFA       STANDARD;      PRT;    58 AA.
AC   Q28280;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Pissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56125; CAA39590.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     58       POTENTIAL.
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6285 MW;  8469D488A2E12DFA CRC64;

  Query Match             40.8%;  Score 62;  DB 1;  Length 58;
  Best Local Similarity   40.6%;  Pred. No. 0.012;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db          7 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 38


RESULT 4
A4_RABIT
ID   A4_RABIT       STANDARD;      PRT;    58 AA.
AC   Q28748;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
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RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56129; CAA39594.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   DOMAIN       58    >58       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6300 MW;  F434209D88EBA82D CRC64;

  Query Match             40.8%;  Score 62;  DB 1;  Length 58;
  Best Local Similarity   40.6%;  Pred. No. 0.012;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db          6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 37


RESULT 5
A4_SHEEP
ID   A4_SHEEP       STANDARD;      PRT;    58 AA.
AC   Q28757;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56130; CAA39595.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   DOMAIN       58    >58       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6300 MW;  F434209D88EBA82D CRC64;

  Query Match             40.8%;  Score 62;  DB 1;  Length 58;
  Best Local Similarity   40.6%;  Pred. No. 0.012;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db          6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 37


RESULT 6
A4_BOVIN
ID   A4_BOVIN       STANDARD;      PRT;    59 AA.
AC   Q28053;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X56124; CAA39589.1; -.
DR   EMBL; X56126; CAA39591.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     58       POTENTIAL.
FT   DOMAIN       59    >59       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      59     59
SQ   SEQUENCE   59 AA;  6414 MW;  F43469D488A2E12D CRC64;

  Query Match             40.8%;  Score 62;  DB 1;  Length 59;
  Best Local Similarity   40.6%;  Pred. No. 0.012;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db          7 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 38


RESULT 7
A4_SAISC
ID   A4_SAISC       STANDARD;      PRT;   751 AA.
AC   Q95241;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
DE   APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
DE   Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
DE   CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Liver;
RX   MEDLINE=96108492; PubMed=8532114;
RA   Levy E., Amorim A., Frangione B., Walker L.C.;
RT   "Beta-amyloid precursor protein gene in squirrel monkeys with
RT   cerebral amyloid angiopathy.";
RL   Neurobiol. Aging 16:805-808(1995).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=Q95241-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q95241-2; Sequence=Not described;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
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CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S81024; AAD14347.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Amyloid; Alternative splicing.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    751       A4 PROTEIN.
FT   CHAIN        18    668       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    652       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       653    751       C99 (POTENTIAL).
FT   CHAIN       653    694       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN       653    692       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN       669    751       C83 (POTENTIAL).
FT   CHAIN       669    694       P3(42) (POTENTIAL).
FT   CHAIN       669    692       P3(40) (POTENTIAL).
FT   CHAIN       693    751       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN       695    751       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN       702    751       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN       721    751       C31 (POTENTIAL).
FT   DOMAIN       18    680       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    681    704       POTENTIAL.
FT   DOMAIN      705    751       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      316    344       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      363    428       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      504    521       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      713    732       INTERACTION WITH G(O)-ALPHA
FT                                (BY SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND.
FT   SITE        652    653       CLEAVAGE (BY BETA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        653    654       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        668    669       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        685    685       INVOLVED IN FREE RADICAL PROPAGATION
FT                                (BY SIMILARITY).
FT   SITE        687    687       INVOLVED IN OXIDATIVE REACTIONS
FT                                (BY SIMILARITY).
FT   SITE        692    693       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                (BY SIMILARITY).
FT   SITE        694    695       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                (BY SIMILARITY).
FT   SITE        701    702       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                (BY SIMILARITY).
FT   SITE        705    715       BASOLATERAL SORTING SIGNAL
FT                                (BY SIMILARITY).
FT   SITE        720    721       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT                                (BY SIMILARITY).
FT   SITE        738    741       ENDOCYTOSIS SIGNAL.
FT   SITE        740    743       NPXY MOTIF.

  Query Match             40.8%;  Score 62;  DB 1;  Length 751;
  Best Local Similarity   40.6%;  Pred. No. 0.19;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db        653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 684


RESULT 8
A4_CAVPO
ID   A4_CAVPO       STANDARD;      PRT;   770 AA.
AC   Q60495; Q60496;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
DE   protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
DE   P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE   CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
GN   APP.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Liver;
RX   MEDLINE=97236426; PubMed=9116031;
RA   Beck M., Mueller D., Bigl V.;
RT   "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT   alternative splicing.";
RL   Biochim. Biophys. Acta 1351:17-21(1997).
RN   [2]
RP   INTERACTION OF BETA-APP40 WITH APOE.
RX   MEDLINE=98007700; PubMed=9349544;
RA   Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
RA   Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
RT   "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
RT   cerebral capillary sequestration and blood-brain barrier transport of
RT   circulating Alzheimer's amyloid beta.";
RL   J. Neurochem. 69:1995-2004(1997).
RN   [3]
RP   PROCESSING.
RX   MEDLINE=20084499; PubMed=10619481;
RA   Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA   Bigl V.;
RT   "Guinea-pig primary cell cultures provide a model to study expression
RT   and amyloidogenic processing of endogenous amyloid precursor
RT   protein.";
RL   Neuroscience 95:243-254(2000).
RN   [4]
RP   GAMMA-SECRETASE PROCESSING.
RX   MEDLINE=20576391; PubMed=11035007;
RA   Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA   Ziani-Cherif C., Onstead L., Sambamurti K.;
RT   "A novel gamma -secretase assay based on detection of the putative
RT   C-terminal fragment-gamma of amyloid beta protein precursor.";
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RL   J. Biol. Chem. 276:481-487(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC       and apoliproteins E and J in the CSF and to HDL particles in
CC       plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) and DDB1 (By similarity).
CC       Associates with microtubules in the presence of ATP and in a
CC       kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC       all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC       ApoE3 appears to be the preferred amyloid binding isoform, while
CC       the apoE4 isoform-beta-APP40 complex is capable of being
CC       transported across the blood-brain barrier.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated pits
CC       (By similarity). During maturation, the immature APP (N-
CC       glycosylated in the endoplasmic reticulum) moves to the Golgi
CC       complex where complete maturation occurs (O-glycosylated and
CC       sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC       APP is released into the extracellular space and the C-terminal is
CC       internalized to endosomes and lysosomes (By similarity). Some APP
CC       accumulates in secretory transport vesicles leaving the late Golgi
CC       compartment and returns to the cell surface (By similarity). APP
CC       sorts to the basolateral surface in epithelial cells (By
CC       similatity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms, missing exons 7,8 and 15, seem to
CC         exist. The L-isoforms, missing exon 15, are referred to as
CC         appicans;
CC       Name=APP770;
CC         IsoId=Q60495-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
CC   -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC       brain. The longer isoforms containing the BPTI domain are
CC       predominantly expressed in peripheral organs such as muscle and
CC       liver.
CC   -!- INDUCTION: Increased levels during neuronal differentiation.
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells.
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue (By similarity). The NPXY site is also involved in
CC       clathrin-mediated endocytosis.
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC       gamma-secretase yields P3 peptides. This is the major secretory
CC       pathway and is nonamyloidogenic. Alternatively,
CC       presenilin/nicastrin-mediated gamma-secretase processing of CTF-
CC       beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC       and amyloid-beta 42 (Abeta42), major components of amyloid
CC       plaques, and the corresponding cytotoxic C-terminal fragments
CC       (CTFs).
CC   -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC       apoptosis (By similarity).
CC   -!- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
CC       the L-APP isoforms produces the APP proteoglycan core proteins,
CC       the appicans (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific (By similarity).
CC       Phosphorylation can affect APP processing, neuronal
CC       differentiation and interaction with other proteins.
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X97631; CAA66230.1; -.
DR   EMBL; X99198; CAA67589.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL       1    17       BY SIMILARITY.
FT   CHAIN       18   770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN       18   687       SOLUBLE APP-ALPHA (BY SIMILARITY).
FT   CHAIN       18   671       SOLUBLE APP-BETA (BY SIMILARITY).
FT   CHAIN      672   770       CTF-ALPHA (BY SIMILARITY).
FT   CHAIN      672   713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN      672   711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
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FT   CHAIN        688    770        CTF-BETA (BY SIMILARITY).
FT   CHAIN        688    713        P3(42) (BY SIMILARITY).
FT   CHAIN        688    711        P3(40) (BY SIMILARITY).
FT   CHAIN        712    770        GAMMA-CTF(59) (BY SIMILARITY).
FT   CHAIN        714    770        GAMMA-CTF(57) (BY SIMILARITY).

  Query Match             40.8%;  Score 62;  DB 1;  Length 770;
  Best Local Similarity   40.6%;  Pred. No. 0.19;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db        672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 703


RESULT 9
A4_HUMAN
ID   A4_HUMAN       STANDARD;      PRT;   770 AA.
AC   P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
AC   Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCC8; Q9UCD1; Q9UQ58;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE   nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE   alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE   (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE   P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE   (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE   secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE   (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE   (Amyloid intracellular domain 50) (AID(50)); C31].
GN   APP OR A4 OR AD1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=87144572; PubMed=2881207;
RA   Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA   Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT   "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT   cell-surface receptor.";
RL   Nature 325:733-736(1987).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM APP751).
RC   TISSUE=Brain;
RX   MEDLINE=88122639; PubMed=2893289;
RA   Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA   Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA   Cordell B.;
RT   "A new A4 amyloid mRNA contains a domain homologous to serine
RT   proteinase inhibitors.";
RL   Nature 331:525-527(1988).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RX   MEDLINE=89128427; PubMed=2783775;
RA   Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA   Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT   "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT   is encoded by 16 exons.";
RL   Nucleic Acids Res. 17:517-522(1989).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM APP770).
RX   MEDLINE=90236318; PubMed=2110105;
RA   Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT   "Genomic organization of the human amyloid beta-protein precursor
RT   gene.";
RL   Gene 87:257-263(1990).
RN   [5]
RP   ERRATUM, AND REVISIONS.
RA   Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RL   Gene 102:291-292(1991).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM L-APP733).
RC   TISSUE=Leukocyte;
RX   MEDLINE=92268136; PubMed=1587857;
RA   Koenig G., Moenning U., Czech C., Prior R., Banati R.,
RA   Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
RT   "Identification and differential expression of a novel alternative
RT   splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
RT   leukocytes and brain microglial cells.";
RL   J. Biol. Chem. 267:10804-10809(1992).
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM APP770).
RX   MEDLINE=97263807; PubMed=9108164;
RA   Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RA   Saito M., Tsukuni S., Sakaki Y.;
RT   "A novel method for making nested deletions and its application for
RT   sequencing of a 300 kb region of human APP locus.";
RL   Nucleic Acids Res. 25:1802-1808(1997).
RN   [8]
RP   SEQUENCE FROM N.A. (ISOFORM APP639).
RC   TISSUE=Brain;
RX   MEDLINE=22744650; PubMed=12859342;
RA   Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
RT   "Identification of a novel alternative splicing isoform of human
RT   amyloid precursor protein gene, APP639.";
RL   Eur. J. Neurosci. 18:102-108(2003).
RN   [9]
RP   SEQUENCE FROM N.A. (ISOFORM APP305).
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [10]
RP   SEQUENCE OF 1-10 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=89016647; PubMed=3140222;
RA   Schon E.A., Mita S., Sadlock J., Herbert J.;
RT   "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT   encodes a 95-kDa polypeptide.";
RL   Nucleic Acids Res. 16:9351-9351(1988).
RN   [11]
RP   ERRATUM, AND REVISIONS.
RA   Mita S., Sadlock J., Herbert J., Schon E.A.;
RL   Nucleic Acids Res. 16:11402-11402(1988).
RN   [12]
RP   SEQUENCE OF 1-75 FROM N.A.
RX   MEDLINE=89165870; PubMed=2538123;
RA   La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
RT   "Characterization of the 5'-end region and the first two exons of the
RT   beta-protein precursor gene.";
RL   Biochem. Biophys. Res. Commun. 159:297-304(1989).
RN   [13]
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RP   SEQUENCE OF 18-50.
RC   TISSUE=Fibroblast;
RX   MEDLINE=87250462; PubMed=3597385;
RA   van Nostrand W.E., Cunningham D.D.;
RT   "Purification of protease nexin II from human fibroblasts.";
RL   J. Biol. Chem. 262:8508-8514(1987).
RN   [14]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
RC   TISSUE=Brain;
RX   MEDLINE=89346754; PubMed=2569763;
RA   de Sauvage F., Octave J.N.;
RT   "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT   secreted protein.";
RL   Science 245:651-653(1989).
RN   [15]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=87231971; PubMed=3035574;
RA   Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT   "Molecular cloning and characterization of a cDNA encoding the
RT   cerebrovascular and the neuritic plaque amyloid peptides.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN   [16]
RP   SEQUENCE OF 286-366 FROM N.A.
RX   MEDLINE=88122640; PubMed=2893290;
RA   Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA   Gusella J.F., Neve R.L.;
RT   "Protease inhibitor domain encoded by an amyloid protein precursor
RT   mRNA associated with Alzheimer's disease.";
RL   Nature 331:528-530(1988).
RN   [17]
RP   SEQUENCE OF 287-367 FROM N.A.
RX   MEDLINE=88122641; PubMed=2893291;
RA   Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT   "Novel precursor of Alzheimer's disease amyloid protein shows
RT   protease inhibitory activity.";
RL   Nature 331:530-532(1988).
RN   [18]
RP   SEQUENCE OF 507-770 FROM N.A.
RC   TISSUE=Brain cortex;
RX   MEDLINE=88124954; PubMed=2893379;
RA   Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA   Marotta C.A.;
RT   "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT   disease brain: coding and noncoding regions of the fetal precursor
RT   mRNA are expressed in the cortex.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN   [19]
RP   SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX   MEDLINE=96139497; PubMed=8576160;
RA   Beher D., Hesse L., Masters C.L., Multhaup G.;
RT   "Regulation of amyloid protein precursor (APP) binding to collagen and
RT   mapping of the binding sites on APP and collagen type I.";
RL   J. Biol. Chem. 271:1613-1620(1996).
RN   [20]
RP   SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717
RP   AND AD GLY-717.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
RN   [21]
RP   SEQUENCE OF 656-737 FROM N.A.
RX   MEDLINE=89392030; PubMed=2675837;
RA   Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA   Little S.P.;
RT   "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT   similarity to soybean trypsin inhibitor.";
RL   Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN   [22]

  Query Match             40.8%;  Score 62;  DB 1;  Length 770;
  Best Local Similarity   40.6%;  Pred. No. 0.19;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db        672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 703


RESULT 10
A4_MACFA
ID   A4_MACFA       STANDARD;      PRT;   770 AA.
AC   P53601; Q95KN7;
DT   01-OCT-1996 (Rel. 34, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC   TISSUE=Cerebellum;
RX   MEDLINE=91273117; PubMed=1905108;
RA   Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT   "Homology of the amyloid beta protein precursor in monkey and human
RT   supports a primate model for beta amyloidosis in Alzheimer's
RT   disease.";
RL   Am. J. Pathol. 138:1423-1435(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
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CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=P53601-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M58727; AAA36829.1; -.
DR   EMBL; M58726; AAA36828.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1    17       BY SIMILARITY.
FT   CHAIN        18   770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18   687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18   671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672   770       C99 (POTENTIAL).
FT   CHAIN       672   713       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN       672   711       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN       688   770       C83 (POTENTIAL).
FT   CHAIN       688   713       P3(42) (POTENTIAL).
FT   CHAIN       688   711       P3(40) (POTENTIAL).
FT   CHAIN       712   770       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN       714   770       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN       721   770       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN       740   770       C31 (POTENTIAL).
FT   DOMAIN       18   699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    700   723       POTENTIAL.
FT   DOMAIN      724   770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96   110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      181   188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291   341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      391   423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      491   522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      523   540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      732   751       INTERACTION WITH G(O)-ALPHA
FT                               (BY SIMILARITY).
FT   DOMAIN      230   260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274   280       POLY-THR.
FT   SITE        144   144       REQUIRED FOR COPPER(II) REDUCTION
FT                               (BY SIMILARITY).
FT   ACT_SITE    301   302       REACTIVE BOND (BY SIMILARITY).
FT   SITE        671   672       CLEAVAGE (BY BETA-SECRETASE)
FT                               (BY SIMILARITY).
FT   SITE        672   673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        687   688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                               (BY SIMILARITY).
FT   SITE        704   704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                               (BY SIMILARITY).
FT   SITE        706   706       INVOLVED IN OXIDATIVE REACTIONS
FT                               (BY SIMILARITY).
FT   SITE        711   712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                               (BY SIMILARITY).
FT   SITE        713   714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                               (BY SIMILARITY).
FT   SITE        720   721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                               (BY SIMILARITY).
FT   SITE        724   734       BASOLATERAL SORTING SIGNAL
FT                               (BY SIMILARITY).
FT   SITE        739   740       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)

  Query Match             40.8%;  Score 62;  DB 1;  Length 770;
  Best Local Similarity   40.6%;  Pred. No. 0.19;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db        672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 703
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RESULT 11
A4_PIG
ID   A4_PIG          STANDARD;      PRT;   770 AA.
AC   P79307; Q29023; Q9TUI0;
DT   01-NOV-1997 (Rel. 35, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura A., Takahashi T.;
RT   "Amyloid precursor protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-136 FROM N.A.
RC   TISSUE=Small intestine;
RA   Winteroe A.K., Fredholm M.;
RT   "Evaluation and characterization of a porcine small intestine cDNA
RT   library.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 667-723 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB032550; BAA84580.1; -.
DR   EMBL; Z84022; CAB06313.1; -.
DR   EMBL; X56127; CAA39592.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
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DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672    770       C99 (BY SIMILARITY).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688    770       C83 (BY SIMILARITY).
FT   CHAIN       688    713       P3(42) (BY SIMILARITY).
FT   CHAIN       688    711       P3(40) (BY SIMILARITY).
FT   CHAIN       712    770       GAMMA-CTF(59).
FT   CHAIN       714    770       GAMMA-CTF(57).
FT   CHAIN       721    770       GAMMA-CTF(50) (BY SIMILARITY).
FT   CHAIN       740    770       C31 (DURING APOPTOSIS) (BY SIMILARITY).
FT   DOMAIN       18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    700    723       POTENTIAL.
FT   DOMAIN      724    770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      135    155       COPPER-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      391    423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      491    522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      523    540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      732    751       INTERACTION WITH G(O)-ALPHA (BY
FT                                SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND (BY SIMILARITY).
FT   SITE        671    672       CLEAVAGE (BY BETA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        672    673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        687    688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        704    704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                                (BY SIMILARITY).
FT   SITE        706    706       INVOLVED IN OXIDATIVE REACTIONS
FT                                (BY SIMILARITY).
FT   SITE        711    712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                (BY SIMILARITY).
FT   SITE        713    714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                (BY SIMILARITY).
FT   SITE        720    721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)

  Query Match             40.8%;  Score 62;  DB 1;  Length 770;
  Best Local Similarity   40.6%;  Pred. No. 0.19;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db        672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 703


RESULT 12
VGLF_RINDB
ID   VGLF_RINDB     STANDARD;      PRT;   546 AA.
AC   P41360;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Rinderpest virus (strain RBT1) (RDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=39007;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95088609; PubMed=7996154;
RA   Evans S.A., Baron M.D., Chamberlain R.W., Goatley L., Barrett T.;
RT   "Nucleotide sequence comparisons of the fusion protein gene from
RT   virulent and attenuated strains of rinderpest virus.";
RL   J. Gen. Virol. 75:3611-3617(1994).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z31656; CAA83482.1; -.
DR   PIR; S47300; S47300.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    546       FUSION GLYCOPROTEIN F0.
FT   CHAIN        20    108       F2 PROTEIN.
FT   CHAIN       109    546       F1 PROTEIN.
FT   DOMAIN      104    108       ARG/LYS-RICH (BASIC).
FT   TRANSMEM    109    133       POTENTIAL.
FT   TRANSMEM    484    513       POTENTIAL.
FT   DOMAIN      514    517       ARG/LYS-RICH (BASIC).
FT   DISULFID     64    191       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD     25     25       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     57     57       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     63     63       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    518    518       O-LINKED (POTENTIAL).
SQ   SEQUENCE   546 AA;  58418 MW;  38B539B89344F401 CRC64;

  Query Match             40.1%;  Score 61;  DB 1;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 0.19;
  Matches   11;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 SITEIKGVIVHRIETILF 30
              |::|||||||||:| : :
Db        283 SLSEIKGVIVHRLEGVSY 300


RESULT 13
VGLF_RINDR
ID   VGLF_RINDR     STANDARD;      PRT;   546 AA.
AC   P41356;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Rinderpest virus (strain RBOK) (RDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
```

```
OX   NCBI_TaxID=36409;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95088609; PubMed=7996154;
RA   Evans S.A., Baron M.D., Chamberlain R.W., Goatley L., Barrett T.;
RT   "Nucleotide sequence comparisons of the fusion protein gene from
RT   virulent and attenuated strains of rinderpest virus.";
RL   J. Gen. Virol. 75:3611-3617(1994).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z30700; CAA83186.1; -.
DR   EMBL; Z30697; CAA83181.1; -.
DR   PIR; S47305; S47305.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    546       FUSION GLYCOPROTEIN F0.
FT   CHAIN        20    108       F2 PROTEIN.
FT   CHAIN       109    546       F1 PROTEIN.
FT   DOMAIN      104    108       ARG/LYS-RICH (BASIC).
FT   TRANSMEM    109    133       POTENTIAL.
FT   TRANSMEM    484    513       POTENTIAL.
FT   DOMAIN      514    517       ARG/LYS-RICH (BASIC).
FT   DISULFID     64    191       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD     25     25       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     57     57       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     63     63       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    518    518       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   546 AA;  58705 MW;  ED3DF8AFFDBECB95 CRC64;

  Query Match             39.5%;  Score 60;  DB 1;  Length 546;
  Best Local Similarity   55.6%;  Pred. No. 0.27;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 SITEIKGVIVHRIETILF 30
              |::||||||:||:| : :
Db        283 SLSEIKGVIIHRLEGVSY 300


RESULT 14
VGLF_CDVO
ID   VGLF_CDVO      STANDARD;      PRT;   662 AA.
AC   P12569; Q65991;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Canine distemper virus (strain Onderstepoort) (CDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11233;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88129050; PubMed=3433924;
RA   Barrett T., Clarke D.K., Evans S.A., Rima B.K.;
RT   "The nucleotide sequence of the gene encoding the F protein of canine
RT   distemper virus: a comparison of the deduced amino acid sequence with
RT   other paramyxoviruses.";
RL   Virus Res. 8:373-386(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93227696; PubMed=8470428;
RA   Wild T.F., Bernard A., Spehner D., Villeval D., Drillien R.;
RT   "Vaccination of mice against canine distemper virus-induced
RT   encephalitis with vaccinia virus recombinants encoding measles or
RT   canine distemper virus antigens.";
RL   Vaccine 11:438-444(1993).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M21849; AAA42878.1; -.
DR   EMBL; X65509; CAA46481.1; -.
DR   PIR; JS0321; VGNZCD.
DR   PIR; S21382; S21382.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL        1      ?
FT   CHAIN         ?    662       FUSION GLYCOPROTEIN F0.
FT   CHAIN         ?    224       PROTEIN F2.
FT   CHAIN       225    662       PROTEIN F1.
FT   TRANSMEM    606    629       POTENTIAL.
FT   DISULFID    180    307       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT      3      3       R -> K (IN REF. 2).
FT   CONFLICT    140    140       D -> N (IN REF. 2).
FT   CONFLICT    152    152       N -> S (IN REF. 2).
FT   CONFLICT    171    171       I -> M (IN REF. 2).
FT   CONFLICT    174    174       A -> V (IN REF. 2).
FT   CONFLICT    662    662       L -> H (IN REF. 2).
SQ   SEQUENCE   662 AA;  72970 MW;  FB2C81C9797805F0 CRC64;

  Query Match             38.8%;  Score 59;  DB 1;  Length 662;
  Best Local Similarity   50.0%;  Pred. No. 0.47;
  Matches    9;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 SITEIKGVIVHRIETILF 30
              :::|:|||||||:| : :
Db        399 TLSEVKGVIVHRLEAVSY 416


RESULT 15
VGLF_MEASY
ID   VGLF_MEASY     STANDARD;      PRT;   534 AA.
AC   P26032;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Measles virus (strain Yamagata-1) (Subacute sclerose panencephalitis
OS   virus).
```

```
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11239;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90385702; PubMed=1698327;
RA   Komase K., Haga T., Yoshikawa Y., Sato T.A., Yamanouchi K.;
RT   "Molecular analysis of structural protein genes of the Yamagata-1
RT   strain of defective subacute sclerosing panencephalitis virus. IV.
RT   Nucleotide sequence of the fusion gene.";
RL   Virus Genes 4:173-181(1990).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D10548; BAA01405.1; -.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL        1     23
FT   CHAIN         24    534       FUSION GLYCOPROTEIN F0.
FT   CHAIN         24    112       PROTEIN F2.
FT   CHAIN        113    534       PROTEIN F1.
FT   TRANSMEM     113    136       POTENTIAL.
FT   DOMAIN       137    494       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     495    515       POTENTIAL.
FT   DOMAIN       516    534       CYTOPLASMIC (POTENTIAL).
FT   DISULFID      68    195       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD      29     29       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      61     61       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      67     67       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   534 AA;  57963 MW;  F5B21757E643844D CRC64;

  Query Match             38.2%;  Score 58;  DB 1;  Length 534;
  Best Local Similarity   55.6%;  Pred. No. 0.53;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 SITEIKGVIVHRIETILF 30
              :::|||||||||:| : :
Db        287 TLSEIKGVIVHRLEGVSY 304


Search completed: June 18, 2004, 19:59:36
Job time : 5.88957 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:15 ; Search time 29.0798 Seconds
(without alignments)
325.503 Million cell updates/sec

Title: US-09-865-294A-71
Perfect score: 152
Sequence: 1 DAEFRHDSGYKISITEIKGVIVHRIETILF 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	64	42.1	82	4	Q16014	Q16014 homo sapien
2	62	40.8	33	4	Q9UC33	Q9uc33 homo sapien
3	62	40.8	82	4	Q16020	Q16020 homo sapien
4	62	40.8	82	4	Q16019	Q16019 homo sapien
5	62	40.8	113	13	Q8JH58	Q8jh58 chelydra se
6	62	40.8	534	13	O93296	O93296 gallus gall
7	62	40.8	569	13	Q9PVL1	Q9pvl1 gallus gall
8	62	40.8	695	13	Q9DGJ8	Q9dgj8 gallus gall
9	62	40.8	751	13	Q9DGJ7	Q9dgj7 gallus gall
10	61	40.1	19	4	Q9UCC8	Q9ucc8 homo sapien
11	61	40.1	28	4	Q9UCD1	Q9ucd1 homo sapien
12	61	40.1	30	4	Q9UCA9	Q9uca9 homo sapien
13	61	40.1	546	12	Q91HA5	Q91ha5 rinderpest
14	60	39.5	546	12	Q84926	Q84926 peste-des-p
15	59.5	39.1	552	12	Q66147	Q66147 cetacean mo
16	59	38.8	528	12	Q9YJW9	Q9yjw9 canine dist
17	59	38.8	530	12	Q8QV06	Q8qv06 canine dist
18	59	38.8	662	12	Q9DXZ2	Q9dxz2 canine dist
19	59	38.8	662	12	Q91KN3	Q91kn3 canine dist
20	59	38.8	662	12	Q9YKL7	Q9ykl7 canine dist
21	59	38.8	662	12	O89327	O89327 canine dist
22	58	38.2	534	12	Q04243	Q04243 measles vir
23	58	38.2	537	12	Q04242	Q04242 measles vir
24	58	38.2	545	12	Q9PXA4	Q9pxa4 measles vir
25	58	38.2	550	12	P90331	P90331 measles vir
26	58	38.2	550	12	Q9QEX0	Q9qex0 measles vir
27	58	38.2	550	12	Q9QEW9	Q9qew9 measles vir
28	58	38.2	550	12	P90330	P90330 measles vir
29	58	38.2	550	12	Q9QEW7	Q9qew7 measles vir
30	58	38.2	550	12	Q9WMK4	Q9wmk4 measles vir
31	58	38.2	550	12	Q89495	Q89495 measles vir
32	58	38.2	550	12	Q8V049	Q8v049 measles vir
33	58	38.2	550	12	Q9YJ94	Q9yj94 measles vir
34	58	38.2	550	12	Q9QEX1	Q9qex1 measles vir
35	58	38.2	550	12	Q9QEW8	Q9qew8 measles vir
36	58	38.2	553	12	O93055	O93055 measles vir
37	58	38.2	553	12	Q9IC36	Q9ic36 measles vir
38	58	38.2	553	12	P88973	P88973 measles vir
39	58	38.2	553	12	Q83536	Q83536 measles vir
40	58	38.2	553	12	O11383	O11383 measles vir
41	58	38.2	553	12	Q9IFK2	Q9ifk2 measles vir
42	58	38.2	553	12	Q83533	Q83533 measles vir
43	58	38.2	553	12	Q83525	Q83525 measles vir
44	58	38.2	553	12	Q83518	Q83518 measles vir
45	58	38.2	553	12	P88974	P88974 measles vir

ALIGNMENTS

RESULT 1
Q16014
ID Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzcwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26263.2; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 8972 MW; P534AA5B3EA9230A CRC64;

Query Match 42.1%; Score 64; DB 4; Length 82;
Best Local Similarity 34.8%; Pred. No. 0.081;
Matches 16; Conservative 6; Mismatches 8; Indels 16; Gaps 2;

```
Qy          1 DAEFRHDSGYKI----------SITEIKGVIVHR------IETILF 30
              ||||||||||::          :   || |:        | |::|
Db         18 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIP 63
```

RESULT 2
Q9UC33

```
ID   Q9UC33      PRELIMINARY;      PRT;    33 AA.
AC   Q9UC33;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=93024877; PubMed=1406936;
RA   Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA   Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT   "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT   biological fluids.";
RL   Nature 359:325-327(1992).
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   33 AA;  3674 MW;  B1DBFE2F4167ABD0 CRC64;

  Query Match             40.8%;  Score 62;  DB 4;  Length 33;
  Best Local Similarity   40.6%;  Pred. No. 0.057;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 32


RESULT 3
Q16020
ID   Q16020      PRELIMINARY;      PRT;    82 AA.
AC   Q16020;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
GN   BETA APP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S61383; AAB26265.2; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8882 MW;  F534AA5AE5D9230A CRC64;

  Query Match             40.8%;  Score 62;  DB 4;  Length 82;
  Best Local Similarity   40.6%;  Pred. No. 0.16;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db         18 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 49


RESULT 4
Q16019
ID   Q16019      PRELIMINARY;      PRT;    82 AA.
AC   Q16019;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
GN   BETA APP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S61380; AAB26264.2; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8938 MW;  F534AA50E579230A CRC64;

  Query Match             40.8%;  Score 62;  DB 4;  Length 82;
  Best Local Similarity   40.6%;  Pred. No. 0.16;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db         18 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 49


RESULT 5
Q8JH58
ID   Q8JH58      PRELIMINARY;      PRT;   113 AA.
AC   Q8JH58;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid beta protein (Fragment).
OS   Chelydra serpentina serpentina (common snapping turtle).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX   NCBI_TaxID=134619;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21876906; PubMed=11882478;
RA   Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT   "Octylphenol (OP) alters the expression of members of the amyloid
RT   protein family in the hypothalamus of the snapping turtle, Chelydra
RT   serpentina serpentina.";
RL   Environ. Health Perspect. 110:269-275(2002).
DR   EMBL; AF541917; AAN04908.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   113 AA;  12750 MW;  72515C930496E053 CRC64;

  Query Match             40.8%;  Score 62;  DB 13;  Length 113;
  Best Local Similarity   40.6%;  Pred. No. 0.23;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db         15 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 46
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RESULT 6
O93296
ID   O93296      PRELIMINARY;      PRT;   534 AA.
AC   O93296;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid protein (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98337885; PubMed=9671674;
RA   Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA   Milligan C.E.;
RT   "Increased production of amyloid precursor protein provides a
RT   substrate for caspase-3 in dying motoneurons.";
RL   J. Neurosci. 18:5869-5880(1998).
DR   EMBL; AF042098; AAC25052.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   534 AA;  60597 MW;  FB53ECC2E66D4C92 CRC64;

  Query Match             40.8%;  Score 62;  DB 13;  Length 534;
  Best Local Similarity   40.6%;  Pred. No. 1.4;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db        436 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 467


RESULT 7
Q9PVL1
ID   Q9PVL1      PRELIMINARY;      PRT;   569 AA.
AC   Q9PVL1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid protein (Fragment).
GN   APP.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUB=Brain;
RA   Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT   "What the evolution of the amyloid protein precursor supergene family
RT   tells us about its function.";
RL   Neurochem. Int. 0:0-0(2000).
DR   EMBL; AF030341; AAF12698.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   569 AA;  64753 MW;  0AB8BB851863A19D CRC64;

  Query Match             40.8%;  Score 62;  DB 13;  Length 569;
  Best Local Similarity   40.6%;  Pred. No. 1.5;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db        472 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 503


RESULT 8
Q9DGJ8
ID   Q9DGJ8      PRELIMINARY;      PRT;   695 AA.
AC   Q9DGJ8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid precursor protein 695 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289218; AAG00593.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   695 AA;  78565 MW;  F201ED02AEC86D95 CRC64;

  Query Match             40.8%;  Score 62;  DB 13;  Length 695;
  Best Local Similarity   40.6%;  Pred. No. 1.9;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 628


RESULT 9
Q9DGJ7
ID   Q9DGJ7      PRELIMINARY;      PRT;   751 AA.
AC   Q9DGJ7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid precursor protein 751 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
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RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289219; AAG00594.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   751 AA;  84705 MW;  E78E9413A8033D84 CRC64;

  Query Match             40.8%;  Score 62;  DB 13;  Length 751;
  Best Local Similarity   40.6%;  Pred. No. 2;
  Matches   13;  Conservative    4;  Mismatches    5;  Indels   10;  Gaps    1;

Qy          1 DAEFRHDSGYKI----------SITEIKGVIV 22
              ||||||||||::          :   || |:
Db        653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAII 684


RESULT 10
Q9UCC8
ID   Q9UCC8      PRELIMINARY;      PRT;    19 AA.
AC   Q9UCC8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid-(1-42) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94068497; PubMed=8248178;
RA   Roher A.E., Lowenson J.D., Clarke S., Woods A.S., Cotter R.J.,
RA   Gowing E., Ball M.J.;
RT   "beta-Amyloid-(1-42) is a major component of cerebrovascular amyloid
RT   deposits: implications for the pathology of Alzheimer disease.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:10836-10840(1993).
DR   HSSP; P05067; 1AMB.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   19 AA;  2315 MW;  05B02B3F6DDECE3E CRC64;

  Query Match             40.1%;  Score 61;  DB 4;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 0.043;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYKI 12
              ||||||||||::
Db          1 DAEFRHDSGYEV 12


RESULT 11
Q9UCD1
ID   Q9UCD1      PRELIMINARY;      PRT;    28 AA.
AC   Q9UCD1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94045685; PubMed=8229004;
RA   Vigo-Pelfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;
RT   "Characterization of beta-amyloid peptide from human cerebrospinal
RT   fluid.";
RL   J. Neurochem. 61:1965-1968(1993).
DR   HSSP; P05067; 1AMB.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   28 AA;  3244 MW;  DE7BD081160AFC81 CRC64;

  Query Match             40.1%;  Score 61;  DB 4;  Length 28;
  Best Local Similarity   83.3%;  Pred. No. 0.067;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYKI 12
              ||||||||||::
Db          1 DAEFRHDSGYEV 12


RESULT 12
Q9UCA9
ID   Q9UCA9      PRELIMINARY;      PRT;    30 AA.
AC   Q9UCA9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94153015; PubMed=8109908;
RA   Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;
RT   "The amino acid sequence of neuritic plaque amyloid from a familial
RT   Alzheimer's disease patient.";
RL   Ann. Neurol. 35:245-246(1994).
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   30 AA;  3391 MW;  FF4167ABD081160A CRC64;

  Query Match             40.1%;  Score 61;  DB 4;  Length 30;
  Best Local Similarity   83.3%;  Pred. No. 0.072;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYKI 12
              ||||||||||::
Db          1 DAEFRHDSGYEV 12


RESULT 13
Q91HA5
ID   Q91HA5      PRELIMINARY;      PRT;   546 AA.
AC   Q91HA5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fusion protein.
GN   F.
OS   Rinderpest virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11241;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K;
RX   MEDLINE=21014265; PubMed=11186456;
RA   Ainaot P.K., Sminev A.G., Bezborodova S.V., Starov S.K., Drygin V.V.,
RA   Gusev A.A.;
RT   "Primary structure of the F-gene from Rinderpest virus strain K.";
RL   Mol. Gen. Mikrobiol. Virusol. 4:29-33(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K;
RA   Ayanot P.K., Sminev A.G., Bezborodova S.V., Starov S.K., Drygin V.V.,
RA   Gusev A.A.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY035887; AAK63190.1; -.
DR   PIR; PQ0866; PQ0866.
DR   PIR; PQ0867; PQ0867.
DR   PIR; PQ0873; PQ0873.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
SQ   SEQUENCE   546 AA;  58572 MW;  449B2B2DD7405F0B CRC64;

  Query Match             40.1%;  Score 61;  DB 12;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 2;
  Matches   11;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 SITEIKGVIVHRIETILF 30
              |::|||||||||:| : :
Db        283 SLSEIKGVIVHRLEGVSY 300


RESULT 14
Q84926
ID   Q84926      PRELIMINARY;      PRT;   546 AA.
AC   Q84926;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fusion protein.
GN   F.
OS   Peste-des-petits-ruminants virus (PPRV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=31604;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VACCINE STRAIN;
RX   MEDLINE=96082318; PubMed=7483819;
RA   Meyer G., Diallo A.;
RT   "The nucleotide sequence of fusion protein gene of the Peste des
RT   petits ruminants virus: the long untranslated region in the 5'end of
RT   the F gene of morbilliviruses seems to be specific to each virus.";
RL   Virus Res. 37:23-35(1995).
DR   EMBL; Z37017; CAA85451.1; -.
DR   PIR; S55386; S55386.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
SQ   SEQUENCE   546 AA;  59310 MW;  DF7D903A4048A0EB CRC64;

  Query Match             39.5%;  Score 60;  DB 12;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 2.8;
  Matches   11;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 SITEIKGVIVHRIETILF 30
              :::|||||||:|| | :
Db        283 TLSEIKGVIVHKIEAISY 300


RESULT 15
Q66147
ID   Q66147      PRELIMINARY;      PRT;   552 AA.
AC   Q66147;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fusion protein precursor.
OS   Cetacean morbillivirus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=36410;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=porpoise;
RX   MEDLINE=95159670; PubMed=7531923;
RA   Bolt G.G.B., Blixenkrone-Moller M.M.B., Gottschalck E., Wishaupt R.G.,
RA   Welsh M.J., Earle J.A.P., Rima B.K.;
RT   "Nucleotide and deduced amino acid sequences of the matrix (M) and
RT   fusion (F) protein genes of cetacean morbilliviruses isolated from a
RT   porpoise and a dolphin.";
RL   Virus Res. 34:291-304(1994).
DR   EMBL; X80757; CAA56731.1; -.
DR   PIR; S47034; S47034.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Signal.
FT   SIGNAL       1     25       POTENTIAL.
SQ   SEQUENCE   552 AA;  60025 MW;  40D9191AD910EA1E CRC64;

  Query Match             39.1%;  Score 59.5;  DB 12;  Length 552;
  Best Local Similarity   41.4%;  Pred. No. 3.4;
  Matches   12;  Conservative    7;  Mismatches    3;  Indels    7;  Gaps    1;

Qy          9 GYKI-------SITEIKGVIVHRIETILF 30
              || |       :::|:|||||||:| : :
Db        278 GYFIVLSIAYPTLSEVKGVIVHRLEAVSY 306


Search completed: June 18, 2004, 20:02:28
Job time : 29.0798 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:20 ; Search time 46.135 Seconds
(without alignments)
195.980 Million cell updates/sec

Title: US-09-865-294A-72
Perfect score: 161
Sequence: 1 DAEFRHDSGYEVKISITEIKGVIVHRIETILF 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	161	100.0	32	6	AAE35678	Aae35678 Human Abe
2	150	93.2	34	6	AAE35679	Aae35679 Human Abe
3	143	88.8	48	6	AAE35680	Aae35680 Human Abe
4	141	87.6	30	6	AAE35677	Aae35677 Human Abe
5	136	84.5	34	6	AAE35681	Aae35681 Human Abe
6	129	80.1	34	6	AAE35682	Aae35682 Human Abe
7	90	55.9	19	6	AAE35657	Aae35657 Measles v
8	90	55.9	31	7	ADD89946	Add89946 CD4 pepti
9	90	55.9	45	7	ADD89951	Add89951 IgE pepti
10	90	55.9	50	7	ADD89944	Add89944 CD4 pepti
11	87	54.0	65	7	ADD89953	Add89953 Foot-and-
12	83	51.6	65	7	ADD89952	Add89952 Foot-and-
13	80	49.7	29	3	AAY91264	Aay91264 Modified
14	80	49.7	60	3	AAY80078	Aay80078 IgE immun
15	79	49.1	29	3	AAY91266	Aay91266 Modified
16	77	47.8	30	3	AAY91262	Aay91262 Modified
17	76	47.2	19	3	AAY68551	Aay68551 Helper T
18	76	47.2	19	3	AAY91135	Aay91135 Modified
19	76	47.2	19	5	ABG68202	Abg68202 Measles v
20	76	47.2	19	5	ABG68208	Abg68208 Measles v
21	76	47.2	19	6	AAE35653	Aae35653 Measles v
22	76	47.2	19	6	AAE35647	Aae35647 Measles v
23	76	47.2	19	6	AAE35644	Aae35644 Measles v
24	76	47.2	29	3	AAY91260	Aay91260 Modified
25	76	47.2	29	3	AAY91258	Aay91258 Modified
26	76	47.2	30	5	ABG68233	Abg68233 Optimised
27	76	47.2	31	3	AAY68582	Aay68582 Peptide i
28	76	47.2	31	3	AAY91173	Aay91173 Modified
29	76	47.2	31	3	AAY91268	Aay91268 Modified
30	76	47.2	32	5	ABG68235	Abg68235 Optimised
31	76	47.2	34	5	ABG68231	Abg68231 Optimised
32	76	47.2	35	3	AAY91242	Aay91242 Modified
33	76	47.2	36	3	AAY91224	Aay91224 Modified
34	76	47.2	36	3	AAY91234	Aay91234 Modified
35	76	47.2	36	3	AAY91238	Aay91238 Modified
36	76	47.2	39	5	ABG68237	Abg68237 Optimised
37	76	47.2	46	3	AAY91240	Aay91240 Modified
38	76	47.2	46	3	AAY91213	Aay91213 Modified
39	76	47.2	46	3	AAY91232	Aay91232 Modified
40	76	47.2	46	3	AAY80020	Aay80020 IgE immun
41	76	47.2	46	5	ABG68229	Abg68229 Optimised
42	76	47.2	46	5	ABG68227	Abg68227 Optimised
43	76	47.2	47	3	AAY68583	Aay68583 Peptide i
44	76	47.2	47	3	AAY91180	Aay91180 Inv epito
45	76	47.2	49	3	AAY91177	Aay91177 Modified

ALIGNMENTS

RESULT 1
AAE35678
ID AAE35678 standard; peptide; 32 AA.
XX
AC AAE35678;
XX
DT 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)
XX
DE Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #2.
XX
KW Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS Homo sapiens.
OS Measles virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1. .12
FT /note= "Human beta amyloid peptide"
FT Region 16. .32
FT /note= "Measles virus T helper cell epitope"
XX
PN WO200296350-A2.
XX
PD 05-DEC-2002.
XX
PF 02-APR-2002; 2002WO-US010293.
XX
PR 25-MAY-2001; 2001US-00865294.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2003-201258/19.
XX
PT Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.
XX
PS Claim 9; Page 39; 77pp; English.
XX
CC The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a

CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 32 AA;

Query Match 100.0%; Score 161; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVKISITEIKGVIVHRIETILF 32
||||||||||||||||||||||||||||||||
Db 1 DAEFRHDSGYEVKISITEIKGVIVHRIETILF 32

RESULT 2
AAE35679
ID AAE35679 standard; peptide; 34 AA.
XX
AC AAE35679;
XX
DT 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)
XX
DE Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #3.
XX
KW Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS Homo sapiens.
OS Measles virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1. .14
FT /note= "Human beta amyloid peptide"
FT Region 18. .34
FT /note= "Measles virus T helper cell epitope"
XX
PN WO200296350-A2.
XX
PD 05-DEC-2002.
XX
PF 02-APR-2002; 2002WO-US010293.
XX
PR 25-MAY-2001; 2001US-00865294.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2003-201258/19.
XX
PT Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.
XX
PS Claim 9; Page 39; 77pp; English.
XX
CC The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 34 AA;

Query Match 93.2%; Score 150; DB 6; Length 34;
Best Local Similarity 94.1%; Pred. No. 3.3e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEV--KISITEIKGVIVHRIETILF 32
|||||||||||| ||||||||||||||||||||
Db 1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34

RESULT 3
AAE35680
ID AAE35680 standard; peptide; 48 AA.
XX
AC AAE35680;
XX
DT 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)
XX
DE Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #4.
XX
KW Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS Homo sapiens.
OS Measles virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1. .28
FT /note= "Human beta amyloid peptide"
FT Region 32. .48
FT /note= "Measles virus T helper cell epitope"
XX
PN WO200296350-A2.
XX
PD 05-DEC-2002.
XX
PF 02-APR-2002; 2002WO-US010293.
XX
PR 25-MAY-2001; 2001US-00865294.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2003-201258/19.
XX
PT Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.
XX
PS Claim 9; Page 39; 77pp; English.

```
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 48 AA;

  Query Match             88.8%;  Score 143;  DB 6;  Length 48;
  Best Local Similarity   66.7%;  Pred. No. 6.5e-15;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels   16;  Gaps    1;

Qy          1 DAEFRHDSGYEV----------------KISITEIKGVIVHRIETILF 32
              ||||||||||||                ||||||||||||||||||||
Db          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48


RESULT 4
AAE35677
ID   AAE35677 standard; peptide; 30 AA.
XX
AC   AAE35677;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #1.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .10
FT                   /note= "Human beta amyloid peptide"
FT   Region          14. .30
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Claim 9; Page 39; 77pp; English.
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 30 AA;

  Query Match             87.6%;  Score 141;  DB 6;  Length 30;
  Best Local Similarity   93.8%;  Pred. No. 7.2e-15;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVKISITEIKGVIVHRIETILF 32
              |||||||||  ||||||||||||||||||||
Db          1 DAEFRHDSGY--KISITEIKGVIVHRIETILF 30


RESULT 5
AAE35681
ID   AAE35681 standard; peptide; 34 AA.
XX
AC   AAE35681;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #5.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .14
FT                   /note= "Human beta amyloid peptide"
FT   Region          18. .34
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
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PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Disclosure; Page 39; 77pp; English.
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 34 AA;

  Query Match             84.5%;  Score 136;  DB 6;  Length 34;
  Best Local Similarity   85.3%;  Pred. No. 5.2e-14;
  Matches   29;  Conservative    2;  Mismatches    1;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEV--KISITEIKGVIVHRIETILF 32
              ||||||||||||  ||||:|||||||:|| |||
Db          1 DAEFRHDSGYEVHHKISISEIKGVIVHKIEGILF 34


RESULT 6
AAE35682
ID   AAE35682 standard; peptide; 34 AA.
XX
AC   AAE35682;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #6.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .14
FT                   /note= "Human beta amyloid peptide"
FT   Region          18. .34
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Disclosure; Page 39; 77pp; English.
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 34 AA;

  Query Match             80.1%;  Score 129;  DB 6;  Length 34;
  Best Local Similarity   85.3%;  Pred. No. 6.6e-13;
  Matches   29;  Conservative    1;  Mismatches    2;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEV--KISITEIKGVIVHRIETILF 32
              ||||||||||||  |||||||: ||| |||||||
Db          1 DAEFRHDSGYEVHHKISITEIRTVIVTRIETILF 34


RESULT 7
AAE35657
ID   AAE35657 standard; peptide; 19 AA.
XX
AC   AAE35657;
XX
DT   17-JUN-2003  (first entry)
XX
DE   Measles virus T helper cell epitope #31.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic.
XX
OS   Measles virus.
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Claim 1; Page 37; 77pp; English.
XX
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CC The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is measles virus T helper (Th) cell epitope used in the
CC exemplification of the invention
XX
SQ Sequence 19 AA;

Query Match 55.9%; Score 90; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ISITEIKGVIVHRIETILF 32
||||||||||||||||||||
Db 1 ISITEIKGVIVHRIETILF 19

RESULT 8
ADD89946
ID ADD89946 standard; protein; 31 AA.
XX
AC ADD89946;
XX
DT 29-JAN-2004 (first entry)
XX
DE CD4 peptide used in immunostimulant complex for anti-HIV vaccine.
XX
KW Immunostimulant; vaccine; human; immunogen; anti-HIV; immunotherapy; CD4.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 20
FT /note= "Epsilon-lysine"
XX
PN WO2003068169-A2.
XX
PD 21-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-US004711.
XX
PR 14-FEB-2002; 2002US-00076674.
PR 31-JAN-2003; 2003US-00076674.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Sokoll KK;
XX
DR WPI; 2003-778890/73.
XX
PT Stabilized immunostimulating complex, useful for vaccination, e.g.
PT against human immune deficiency viruses, comprises cationic peptide
PT immunogen and anionic oligonucleotide.
XX
PS Claim 14; SEQ ID NO 6; 159pp; English.
XX
CC The present sequence is that of a synthetic immunogenic peptide derived
CC from human CD4. This is an example of peptides that can be used in
CC claimed immunostimulatory complexes of the invention that are
CC specifically adapted to act as adjuvant and as peptide immunogen
CC stabiliser. The complexes comprise a CpG oligonucleotide and a
CC biologically active peptide immunogen. The complex is particulate and can
CC efficiently present peptide immunogens to the cells of the immune system
CC to produce an immune response. The complexes may be prepared with various
CC ratios of peptides to CpG oligonucleotides to provide different physical
CC properties, such as the size of the microparticle. An immunostimulatory
CC complex comprising the present CD4 derived peptide can be used in an anti
CC -CD4 immunotherapeutic vaccine for the treatment of HIV infection.
XX
SQ Sequence 31 AA;

Query Match 55.9%; Score 90; DB 7; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ISITEIKGVIVHRIETILF 32
||||||||||||||||||||
Db 1 ISITEIKGVIVHRIETILF 19

RESULT 9
ADD89951
ID ADD89951 standard; protein; 45 AA.
XX
AC ADD89951;
XX
DT 29-JAN-2004 (first entry)
XX
DE IgE peptide used in immunostimulant complex for allergy vaccine.
XX
KW Immunostimulant; vaccine; human; immunogen; IgE; immunotherapy; allergy;
KW antibody; antiallergic.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 20
FT /note= "Epsilon-lysine"
XX
PN WO2003068169-A2.
XX
PD 21-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-US004711.
XX
PR 14-FEB-2002; 2002US-00076674.
PR 31-JAN-2003; 2003US-00076674.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Sokoll KK;
XX
DR WPI; 2003-778890/73.
XX
PT Stabilized immunostimulating complex, useful for vaccination, e.g.
PT against human immune deficiency viruses, comprises cationic peptide
PT immunogen and anionic oligonucleotide.
XX
PS Claim 20; SEQ ID NO 11; 159pp; English.
XX
CC The present sequence is that of a synthetic immunogenic peptide derived
CC from human IgE. This is an example of peptides that can be used in
CC claimed immunostimulatory complexes of the invention that are
CC specifically adapted to act as adjuvant and as peptide immunogen
CC stabiliser. The complexes comprise a CpG oligonucleotide and a
CC biologically active peptide immunogen. The complex is particulate and can
CC efficiently present peptide immunogens to the cells of the immune system
CC to produce an immune response. The complexes may be prepared with various
CC ratios of peptides to CpG oligonucleotides to provide different physical
CC properties, such as the size of the microparticle. An immunostimulatory
CC complex comprising the present IgE derived peptide can be used in an anti
CC -IgE immunotherapeutic vaccine for the treatment of allergy.

```
XX
SQ   Sequence 45 AA;

  Query Match            55.9%;  Score 90;  DB 7;  Length 45;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 10
ADD89944
ID   ADD89944 standard; protein; 50 AA.
XX
AC   ADD89944;
XX
DT   29-JAN-2004  (first entry)
XX
DE   CD4  peptide used in immunostimulant complex as anti-HIV vaccine.
XX
KW   Immunostimulant; vaccine; human; immunogen; anti-HIV; immunotherapy.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   20
FT                   /note= "Epsilon-lysine"
XX
PN   WO2003068169-A2.
XX
PD   21-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004711.
XX
PR   14-FEB-2002; 2002US-00076674.
PR   31-JAN-2003; 2003US-00076674.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Sokoll KK;
XX
DR   WPI; 2003-778890/73.
XX
PT   Stabilized immunostimulating complex, useful for vaccination, e.g.
PT   against human immune deficiency viruses, comprises cationic peptide
PT   immunogen and anionic oligonucleotide.
XX
PS   Claim 14; SEQ ID NO 4; 159pp; English.
XX
CC   The present sequence is that of a synthetic immunogenic peptide derived
CC   from human CD4. This is an example of peptides that can be used in
CC   claimed immunostimulatory complexes of the invention that are
CC   specifically adapted to act as adjuvant and as peptide immunogen
CC   stabiliser. The complexes comprise a CpG oligonucleotide and a
CC   biologically active peptide immunogen. The complex is particulate and can
CC   efficiently present peptide immunogens to the cells of the immune system
CC   to produce an immune response. The complexes may be prepared with various
CC   ratios of peptides to CpG oligonucleotides to provide different physical
CC   properties, such as the size of the microparticle. An immunostimulatory
CC   complex comprising the present CD4 derived peptide can be used in an anti
CC   -CD4 immunotherapeutic vaccine for the treatment of HIV infection.
XX
SQ   Sequence 50 AA;

  Query Match            55.9%;  Score 90;  DB 7;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 11
ADD89953
ID   ADD89953 standard; protein; 65 AA.
XX
AC   ADD89953;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Foot-and-mouth disease peptide used in vaccine immunostimulant complex.
XX
KW   Immunostimulant; vaccine; immunogen; immunotherapy;
KW   foot-and-mouth disease.
XX
OS   Synthetic.
OS   Foot-and-mouth disease virus.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   20
FT                   /note= "Epsilon-lysine"
XX
PN   WO2003068169-A2.
XX
PD   21-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004711.
XX
PR   14-FEB-2002; 2002US-00076674.
PR   31-JAN-2003; 2003US-00076674.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Sokoll KK;
XX
DR   WPI; 2003-778890/73.
XX
PT   Stabilized immunostimulating complex, useful for vaccination, e.g.
PT   against human immune deficiency viruses, comprises cationic peptide
PT   immunogen and anionic oligonucleotide.
XX
PS   Claim 22; SEQ ID NO 13; 159pp; English.
XX
CC   The present sequence is that of a synthetic immunogenic peptide derived
CC   from foot-and-mouth disease (FMD) virus. This is an example of peptides
CC   that can be used in claimed immunostimulatory complexes of the invention
CC   that are specifically adapted to act as adjuvant and as peptide immunogen
CC   stabiliser. The complexes comprise a CpG oligonucleotide and a
CC   biologically active peptide immunogen. The complex is particulate and can
CC   efficiently present peptide immunogens to the cells of the immune system
CC   to produce an immune response. The complexes may be prepared with various
CC   ratios of peptides to CpG oligonucleotides to provide different physical
CC   properties, such as the size of the microparticle. An immunostimulatory
CC   complex comprising the present FMD virus derived peptide can be used in
CC   an anti-FMD vaccine for protective immunity against FMD.
XX
SQ   Sequence 65 AA;

  Query Match            54.0%;  Score 87;  DB 7;  Length 65;
  Best Local Similarity  94.7%;  Pred. No. 6.5e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||||||||||||:||||||
Db          1 ISITEIKGVIVHKIETILF 19


RESULT 12
ADD89952
ID   ADD89952 standard; protein; 65 AA.
XX
AC   ADD89952;
```

XX
DT 29-JAN-2004 (first entry)
XX
DE Foot-and-mouth disease peptide used in vaccine immunostimulant complex.
XX
KW Immunostimulant; vaccine; immunogen; immunotherapy;
KW foot-and-mouth disease.
XX
OS Synthetic.
OS Foot-and-mouth disease virus.
XX
FH Key Location/Qualifiers
FT Modified-site 20
FT /note= "Epsilon-lysine"
XX
PN WO2003068169-A2.
XX
PD 21-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-US004711.
XX
PR 14-FEB-2002; 2002US-00076674.
PR 31-JAN-2003; 2003US-00076674.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Sokoll KK;
XX
DR WPI; 2003-778890/73.
XX
PT Stabilized immunostimulating complex, useful for vaccination, e.g.
PT against human immune deficiency viruses, comprises cationic peptide
PT immunogen and anionic oligonucleotide.
XX
PS Claim 22; SEQ ID NO 12; 159pp; English.
XX
CC The present sequence is that of a synthetic immunogenic peptide derived
CC from foot-and-mouth disease (FMD) virus. This is an example of peptides
CC that can be used in claimed immunostimulatory complexes of the invention
CC that are specifically adapted to act as adjuvant and as peptide immunogen
CC stabiliser. The complexes comprise a CpG oligonucleotide and a
CC biologically active peptide immunogen. The complex is particulate and can
CC efficiently present peptide immunogens to the cells of the immune system
CC to produce an immune response. The complexes may be prepared with various
CC ratios of peptides to CpG oligonucleotides to provide different physical
CC properties, such as the size of the microparticle. An immunostimulatory
CC complex comprising the present FMD virus derived peptide can be used in
CC an anti-FMD vaccine for protective immunity against FMD.
XX
SQ Sequence 65 AA;

Query Match 51.6%; Score 83; DB 7; Length 65;
Best Local Similarity 89.5%; Pred. No. 2.8e-05;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ISITEIKGVIVHRIETILF 32
||||:|||||||:||||||
Db 1 ISISEIKGVIVHKIETILF 19

RESULT 13
AAY91264
ID AAY91264 standard; peptide; 29 AA.
XX
AC AAY91264;
XX
DT 12-SEP-2003 (revised)
DT 22-MAY-2000 (first entry)
XX
DE Modified MVF Th epitope/HIV epitope, SEQ ID NO:142.
XX
KW Promiscuous T-cell epitope; measles virus F protein; MVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KW cholesteryl ester transport protein; anti-arteriosclerotic.
XX
OS Measles virus.
OS Human immunodeficiency virus 1.
OS Chimeric.
XX
PN WO9966957-A2.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US013975.
XX
PR 20-JUN-1998; 98US-00100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus.
XX
PS Claim 13; Page 63; 129pp; English.
XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and immunocastration)
CC ; for promoting the growth of animals; or for treating allergies or
CC arteriosclerosis. Incorporation of a promiscuous Th (functional in
CC genetically diverse subjects) into an immunogen improves capacity to
CC induce a strong T helper cell-mediated immune response, resulting in
CC production of antibodies against a target antigen. Th can replace carrier
CC proteins and pathogen-derived T helper epitopes. Sequence AAY91121
CC represents a promiscuous T helper epitope from the measles virus F (MVF)
CC protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246
CC represent synthetic Th epitopes based on the MVF Th epitope. Sequence
CC AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)
CC surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes
CC derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-
CC Y91244 are antigenic peptides comprising an LHRH sequence joined to a
CC promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide
CC used in these LHRH antigenic peptides. AAY91200 is somatostatin, and
CC AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th
CC epitope. Somatostatin immunogens may be used to promote growth in
CC livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and
CC AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may
CC be used to prevent HIV infection of T cells. AAY90212 is a modified
CC version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219
CC are Th epitope/IgE CH3 antigenic peptides which may be used in the
CC treatment of allergies. AAY91220 is a peptide derived from foot and mouth
CC disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this
CC peptide and a Th epitope. AAY91223 is a Plasmodium falciparum
CC circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS
CC antigen and an MVF Th epitope and may be used in a malaria vaccine.
CC AAY91228-Y91231 represent CETP-derived peptides and AAY91232-Y91241 are
CC immunogens comprising a CETP peptide and a Th epitope which may be used
CC to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247
CC and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-

```
CC   Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and
CC   HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1
CC   vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory
CC   invasin protein epitope from Yersinia species, and hinge spacer peptide,
CC   both of which may optionally be used in the antigenic peptides of the
CC   invention. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ   Sequence 29 AA;

  Query Match             49.7%;  Score 80;  DB 3;  Length 29;
  Best Local Similarity   70.8%;  Pred. No. 2.8e-05;
  Matches   17;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 GYEVKISITEIKGVIVHRIETILF 32
              | :  |||:||||||||:|| |||
Db          6 GPQTXISISEIKGVIVHKIEGILF 29


RESULT 14
AAY80078
ID   AAY80078 standard; peptide; 60 AA.
XX
AC   AAY80078;
XX
DT   15-MAY-2000  (first entry)
XX
DE   IgE immunogenic peptide conjugate SEQ ID NO:85.
XX
KW   Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW   immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW   antibody; allergy; allergic disease; immunisation; anti-allergic;
KW   anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
OS   Unidentified.
XX
PN   WO9967293-A1.
XX
PD   29-DEC-1999.
XX
PF   21-JUN-1999;   99WO-US013959.
XX
PR   20-JUN-1998;   98US-00100287.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY,  Walfield AM;
XX
DR   WPI; 2000-160578/14.
XX
PT   New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT   for immunization against allergy.
XX
PS   Claim 14; Page 76; 155pp; English.
XX
CC   The present invention describes immunoglobulin E (IgE)-CH3 domain
CC   antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
CC   anti-asthmatic properties. (I) induces polyclonal antibodies specific for
CC   a target effector site on the epsilon-heavy chain of IgE, and so
CC   preventing triggering and activation of mast cells and basophils and
CC   downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC   containing (I) are used for active immunisation against IgE-mediated
CC   allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC   dermatitis. Nucleic acids that encode these compounds are useful for
CC   recombinant production of corresponding peptides or in DNA vaccines.
CC   Conjugates of (I) that include a promiscuous T helper cell epitope
CC   (functional in genetically diverse subjects), in addition to a B cell
CC   target epitope, have increased immunogenicity and may include cyclic
CC   constraints (disulfide bridge) to stabilise conformational features and
CC   maximize cross-reactivity to the natural target. They induce safe (non-
CC   anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 60 AA;

  Query Match             49.7%;  Score 80;  DB 3;  Length 60;
  Best Local Similarity   75.0%;  Pred. No. 7.4e-05;
  Matches   18;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 GYEVKISITEIKGVIVHRIETILF 32
              | |  |||:||||||||:|| |||
Db         10 GKEGGISISEIKGVIVHKIEGILF 33


RESULT 15
AAY91266
ID   AAY91266 standard; peptide; 29 AA.
XX
AC   AAY91266;
XX
DT   12-SEP-2003  (revised)
DT   22-MAY-2000  (first entry)
XX
DE   Modified MVF Th epitope/HIV epitope, SEQ ID NO:144.
XX
KW   Promiscuous T-cell epitope; measles virus F protein; MVF;
KW   hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW   luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW   somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW   foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW   Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KW   cholesteryl ester transport protein; anti-arteriosclerotic.
XX
OS   Measles virus.
OS   Human immunodeficiency virus 1.
OS   Chimeric.
XX
PN   WO9966957-A2.
XX
PD   29-DEC-1999.
XX
PF   21-JUN-1999;   99WO-US013975.
XX
PR   20-JUN-1998;   98US-00100412.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2000-160564/14.
XX
PT   New artificial T helper cell epitope and derived immunogens with target
PT   antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT   or human immune deficiency virus.
XX
PS   Claim 13; Page 63; 129pp; English.
XX
CC   The invention relates to novel promiscuous T helper cell epitopes (Th),
CC   and immunogenic peptides comprising the Th epitopes of the invention
CC   along with B cell epitopes. The Th epitopes and peptide immunogens
CC   containing them, are used to induce a T helper cell response,
CC   specifically against Plasmodium falciparum, cholesteryl ester transport
CC   protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC   immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC   peptide immunogens may be used for prevention and/or treatment of
CC   infections (HIV, foot-and-mouth disease or malaria); for cancer
CC   immunotherapy; for inhibition of the action of luteinising hormone
CC   releasing hormone (LHRH) for contraception, treatment of hormone-
CC   dependent cancer, prevention of boar taint in meat, and immunocastration)
CC   ; for promoting the growth of animals; or for treating allergies or
CC   arteriosclerosis. Incorporation of a promiscuous Th (functional in
CC   genetically diverse subjects) into an immunogen improves capacity to
CC   induce a strong T helper cell-mediated immune response, resulting in
CC   production of antibodies against a target antigen. Th can replace carrier
CC   proteins and pathogen-derived T helper epitopes. Sequence AAY91121
CC   represents a promiscuous T helper epitope from the measles virus F (MVF)
CC   protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246
```

CC represent synthetic Th epitopes based on the MVF Th epitope. Sequence
CC AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)
CC surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes
CC derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-
CC Y91244 are antigenic peptides comprising an LHRH sequence joined to a
CC promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide
CC used in these LHRH antigenic peptides. AAY91200 is somatostatin, and
CC AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th
CC epitope. Somatostatin immunogens may be used to promote growth in
CC livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and
CC AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may
CC be used to prevent HIV infection of T cells. AAY90212 is a modified
CC version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219
CC are Th epitope/IgE CH3 antigenic peptides which may be used in the
CC treatment of allergies. AAY91220 is a peptide derived from foot and mouth
CC disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this
CC peptide and a Th epitope. AAY91223 is a Plasmodium falciparum
CC circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS
CC antigen and an MVF Th epitope and may be used in a malaria vaccine.
CC AAY91228-Y91231 represent CETP-derived peptides and AAY91232-Y91241 are
CC immunogens comprising a CETP peptide and a Th epitope which may be used
CC to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247
CC and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-
CC Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and
CC HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1
CC vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory
CC invasin protein epitope from Yersinia species, and hinge spacer peptide,
CC both of which may optionally be used in the antigenic peptides of the
CC invention. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 29 AA;

Query Match 49.1%; Score 79; DB 3; Length 29;
Best Local Similarity 81.0%; Pred. No. 4.1e-05;
Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy         12 VKISITEIKGVIVHRIETILF 32
              | |||:|||||||:|| |||
Db          9 VKISISEIKGVIVHKIEGILF 29
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Search completed: June 18, 2004, 19:58:51
Job time : 46.135 secs

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:54:46 ; Search time 12.5644 Seconds
(without alignments)
131.485 Million cell updates/sec

Title: US-09-865-294A-72
Perfect score: 161
Sequence: 1 DABFRHDSGYEVKISITEIKGVIVHRIETILF 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	76	47.2	19	3	US-09-100-414B-15	Sequence 15, Appl
2	76	47.2	19	3	US-09-303-323-15	Sequence 15, Appl
3	76	47.2	19	4	US-09-770-014-15	Sequence 15, Appl
4	76	47.2	31	3	US-09-100-414B-53	Sequence 53, Appl
5	76	47.2	31	3	US-09-303-323-53	Sequence 53, Appl
6	76	47.2	31	4	US-09-770-014-53	Sequence 53, Appl
7	76	47.2	35	3	US-09-100-414B-80	Sequence 80, Appl
8	76	47.2	35	3	US-09-303-323-80	Sequence 80, Appl
9	76	47.2	35	4	US-09-770-014-80	Sequence 80, Appl
10	76	47.2	46	3	US-09-100-414B-96	Sequence 96, Appl
11	76	47.2	46	3	US-09-303-323-96	Sequence 96, Appl
12	76	47.2	46	4	US-09-770-014-96	Sequence 96, Appl
13	76	47.2	47	3	US-09-100-414B-60	Sequence 60, Appl
14	76	47.2	47	3	US-09-303-323-60	Sequence 60, Appl
15	76	47.2	47	4	US-09-770-014-60	Sequence 60, Appl
16	76	47.2	49	3	US-09-100-414B-57	Sequence 57, Appl
17	76	47.2	49	3	US-09-303-323-57	Sequence 57, Appl
18	76	47.2	49	4	US-09-770-014-57	Sequence 57, Appl
19	76	47.2	80	3	US-09-100-600A-30	Sequence 30, Appl
20	72.5	45.0	35	2	US-08-612-785B-15	Sequence 15, Appl
21	72.5	45.0	35	4	US-08-617-267C-15	Sequence 15, Appl
22	71.5	44.4	35	2	US-08-612-785B-39	Sequence 39, Appl
23	71	44.1	19	3	US-09-100-414B-17	Sequence 17, Appl
24	71	44.1	19	3	US-09-303-323-17	Sequence 17, Appl
25	71	44.1	19	4	US-09-770-014-17	Sequence 17, Appl
26	71	44.1	31	3	US-09-100-414B-55	Sequence 55, Appl
27	71	44.1	31	3	US-09-303-323-55	Sequence 55, Appl
28	71	44.1	31	4	US-09-770-014-55	Sequence 55, Appl
29	69	42.9	19	3	US-09-100-414B-18	Sequence 18, Appl
30	69	42.9	19	3	US-09-100-414B-19	Sequence 19, Appl
31	69	42.9	19	3	US-09-100-414B-20	Sequence 20, Appl
32	69	42.9	19	3	US-09-303-323-18	Sequence 18, Appl
33	69	42.9	19	3	US-09-303-323-19	Sequence 19, Appl
34	69	42.9	19	3	US-09-303-323-20	Sequence 20, Appl
35	69	42.9	19	4	US-09-770-014-18	Sequence 18, Appl
36	69	42.9	19	4	US-09-770-014-19	Sequence 19, Appl
37	69	42.9	19	4	US-09-770-014-20	Sequence 20, Appl
38	69	42.9	31	3	US-09-100-414B-56	Sequence 56, Appl
39	69	42.9	31	3	US-09-100-414B-59	Sequence 59, Appl
40	69	42.9	31	3	US-09-100-414B-61	Sequence 61, Appl
41	69	42.9	31	3	US-09-303-323-56	Sequence 56, Appl
42	69	42.9	31	3	US-09-303-323-59	Sequence 59, Appl
43	69	42.9	31	3	US-09-303-323-61	Sequence 61, Appl
44	69	42.9	31	4	US-09-770-014-56	Sequence 56, Appl
45	69	42.9	31	4	US-09-770-014-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-100-414B-15
; Sequence 15, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-15

Query Match 47.2%; Score 76; DB 3; Length 19;
Best Local Similarity 84.2%; Pred. No. 1e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy         14 ISITEIKGVIVHRIETILF 32
              |||:|||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19
```

RESULT 2

```
US-09-303-323-15
; Sequence 15, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/303,323
;      FILING DATE:  30-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-303-323-15

  Query Match             47.2%;  Score 76;  DB 3;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 1e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||:||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 3
US-09-770-014-15
; Sequence 15, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/770,014
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-15

  Query Match             47.2%;  Score 76;  DB 4;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 1e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||:||||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 4
US-09-100-414B-53
; Sequence 53, Application US/09100414B
; Patent No. 6025468
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/100,414B
;      FILING DATE:  20-JUNE-1998
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-100-414B-53

  Query Match             47.2%;  Score 76;  DB 3;  Length 31;
  Best Local Similarity   84.2%;  Pred. No. 1.9e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;
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```
Qy          14 ISITEIKGVIVHRIETILF 32
               |||:|||||||:|| |||
Db           1 ISISEIKGVIVHKIEGILF 19


RESULT 5
US-09-303-323-53
; Sequence 53, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/303,323
;      FILING DATE:  30-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-303-323-53

  Query Match             47.2%;  Score 76;  DB 3;  Length 31;
  Best Local Similarity   84.2%;  Pred. No. 1.9e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          14 ISITEIKGVIVHRIETILF 32
               |||:|||||||:|| |||
Db           1 ISISEIKGVIVHKIEGILF 19


RESULT 6
US-09-770-014-53
; Sequence 53, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/770,014
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-53

  Query Match             47.2%;  Score 76;  DB 4;  Length 31;
  Best Local Similarity   84.2%;  Pred. No. 1.9e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          14 ISITEIKGVIVHRIETILF 32
               |||:|||||||:|| |||
Db           1 ISISEIKGVIVHKIEGILF 19


RESULT 7
US-09-100-414B-80
; Sequence 80, Application US/09100414B
; Patent No. 6025468
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/100,414B
;      FILING DATE:  20-JUNE-1998
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  80:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-100-414B-80

  Query Match             47.2%;  Score 76;  DB 3;  Length 35;
  Best Local Similarity   84.2%;  Pred. No. 2.2e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||:|||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 8
US-09-303-323-80
; Sequence 80, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/303,323
;      FILING DATE:  30-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  80:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-303-323-80

  Query Match             47.2%;  Score 76;  DB 3;  Length 35;
  Best Local Similarity   84.2%;  Pred. No. 2.2e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||:|||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 9
US-09-770-014-80
; Sequence 80, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/770,014
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  80:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-80

  Query Match             47.2%;  Score 76;  DB 4;  Length 35;
  Best Local Similarity   84.2%;  Pred. No. 2.2e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||:|||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 10
US-09-100-414B-96
; Sequence 96, Application US/09100414B
; Patent No. 6025468
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/100,414B
;      FILING DATE:  20-JUNE-1998
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  96:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  46 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-100-414B-96

  Query Match             47.2%;  Score 76;  DB 3;  Length 46;
  Best Local Similarity   84.2%;  Pred. No. 3.1e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||:|||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 11
US-09-303-323-96
; Sequence 96, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/303,323
;      FILING DATE:  30-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  96:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  46 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-303-323-96

  Query Match             47.2%;  Score 76;  DB 3;  Length 46;
  Best Local Similarity   84.2%;  Pred. No. 3.1e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||:|||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 12
US-09-770-014-96
; Sequence 96, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/770,014
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  96:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  46 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-96

  Query Match             47.2%;  Score 76;  DB 4;  Length 46;
  Best Local Similarity   84.2%;  Pred. No. 3.1e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||:|||||||:|| |||
Db          1 ISISEIKGVIVHKIEGILF 19


RESULT 13
US-09-100-414B-60
; Sequence 60, Application US/09100414B
; Patent No. 6025468
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
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```
;       APPLICATION NUMBER:  US/09/100,414B
;       FILING DATE:  20-JUNE-1998
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Maria H. Lin
;       REGISTRATION NUMBER:  29,323
;       REFERENCE/DOCKET NUMBER:  1151-4157
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212-758-4800
;       TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  60:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  47 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-09-100-414B-60

  Query Match             47.2%;  Score 76;  DB 3;  Length 47;
  Best Local Similarity   84.2%;  Pred. No. 3.2e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||:||||||||:|| |||
Db         17 ISISEIKGVIVHKIEGILF 35


RESULT 14
US-09-303-323-60
; Sequence 60, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/303,323
;      FILING DATE:  30-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  47 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-303-323-60

  Query Match             47.2%;  Score 76;  DB 3;  Length 47;
  Best Local Similarity   84.2%;  Pred. No. 3.2e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||:||||||||:|| |||
Db         17 ISISEIKGVIVHKIEGILF 35


RESULT 15
US-09-770-014-60
; Sequence 60, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/770,014
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  47 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-60

  Query Match             47.2%;  Score 76;  DB 4;  Length 47;
  Best Local Similarity   84.2%;  Pred. No. 3.2e-05;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||:||||||||:|| |||
Db         17 ISISEIKGVIVHKIEGILF 35


Search completed: June 18, 2004, 20:04:45
Job time : 12.5644 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 20:02:36 ; Search time 36.1227 Seconds
(without alignments)
250.093 Million cell updates/sec

Title: US-09-865-294A-72
Perfect score: 161
Sequence: 1 DAEFRHDSGYEVKISITEIKGVIVHRIETILF 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	161	100.0	32	10	US-09-865-294-72	Sequence 72, Appl
2	150	93.2	34	10	US-09-865-294-73	Sequence 73, Appl
3	143	88.8	48	10	US-09-865-294-74	Sequence 74, Appl
4	141	87.6	30	10	US-09-865-294-71	Sequence 71, Appl
5	136	84.5	34	10	US-09-865-294-75	Sequence 75, Appl
6	129	80.1	34	10	US-09-865-294-76	Sequence 76, Appl
7	90	55.9	19	10	US-09-865-294-51	Sequence 51, Appl
8	90	55.9	31	14	US-10-076-674-6	Sequence 6, Appli
9	90	55.9	31	15	US-10-355-161A-6	Sequence 6, Appli
10	90	55.9	45	14	US-10-076-674-11	Sequence 11, Appl
11	90	55.9	45	15	US-10-355-161A-11	Sequence 11, Appl
12	90	55.9	50	14	US-10-076-674-4	Sequence 4, Appli
13	90	55.9	50	15	US-10-355-161A-4	Sequence 4, Appli
14	87	54.0	65	15	US-10-355-161A-13	Sequence 13, Appl
15	83	51.6	65	15	US-10-355-161A-12	Sequence 12, Appl
16	76	47.2	19	10	US-09-747-802-49	Sequence 49, Appl
17	76	47.2	19	10	US-09-747-802-55	Sequence 55, Appl
18	76	47.2	19	10	US-09-865-294-38	Sequence 38, Appl
19	76	47.2	19	10	US-09-865-294-41	Sequence 41, Appl
20	76	47.2	19	10	US-09-865-294-47	Sequence 47, Appl
21	76	47.2	30	10	US-09-747-802-80	Sequence 80, Appl
22	76	47.2	32	10	US-09-747-802-82	Sequence 82, Appl
23	76	47.2	34	10	US-09-747-802-78	Sequence 78, Appl
24	76	47.2	39	10	US-09-747-802-84	Sequence 84, Appl
25	76	47.2	46	10	US-09-747-802-74	Sequence 74, Appl
26	76	47.2	46	10	US-09-747-802-76	Sequence 76, Appl
27	72.5	45.0	35	9	US-09-972-475-15	Sequence 15, Appl
28	72.5	45.0	35	15	US-10-463-729-15	Sequence 15, Appl
29	71	44.1	19	10	US-09-747-802-48	Sequence 48, Appl
30	71	44.1	19	10	US-09-865-294-40	Sequence 40, Appl
31	69	42.9	19	10	US-09-747-802-46	Sequence 46, Appl
32	69	42.9	19	10	US-09-747-802-50	Sequence 50, Appl
33	69	42.9	19	10	US-09-747-802-51	Sequence 51, Appl
34	69	42.9	19	10	US-09-747-802-54	Sequence 54, Appl
35	69	42.9	19	10	US-09-747-802-56	Sequence 56, Appl
36	69	42.9	19	10	US-09-865-294-42	Sequence 42, Appl
37	69	42.9	19	10	US-09-865-294-43	Sequence 43, Appl
38	69	42.9	19	10	US-09-865-294-46	Sequence 46, Appl
39	69	42.9	19	10	US-09-865-294-48	Sequence 48, Appl
40	69	42.9	30	10	US-09-747-802-81	Sequence 81, Appl
41	69	42.9	32	10	US-09-747-802-83	Sequence 83, Appl
42	69	42.9	34	10	US-09-747-802-79	Sequence 79, Appl
43	69	42.9	39	10	US-09-747-802-85	Sequence 85, Appl
44	69	42.9	46	10	US-09-747-802-75	Sequence 75, Appl
45	69	42.9	46	10	US-09-747-802-77	Sequence 77, Appl

ALIGNMENTS

RESULT 1
US-09-865-294-72
; Sequence 72, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Measles virus
US-09-865-294-72

Query Match 100.0%; Score 161; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVKISITEIKGVIVHRIETILF 32
||||||||||||||||||||||||||||||||
Db 1 DAEFRHDSGYEVKISITEIKGVIVHRIETILF 32

RESULT 2
US-09-865-294-73
; Sequence 73, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294

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;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
;    LENGTH: 34
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-73

  Query Match             93.2%;  Score 150;  DB 10;  Length 34;
  Best Local Similarity   94.1%;  Pred. No. 1.1e-15;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEV--KISITEIKGVIVHRIETILF 32
              ||||||||||||  ||||||||||||||||||||
Db          1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34


RESULT 3
US-09-865-294-74
; Sequence 74, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
;    LENGTH: 48
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-74

  Query Match             88.8%;  Score 143;  DB 10;  Length 48;
  Best Local Similarity   66.7%;  Pred. No. 1.9e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels   16;  Gaps    1;

Qy          1 DAEFRHDSGYEV----------------KISITEIKGVIVHRIETILF 32
              ||||||||||||                ||||||||||||||||||||
Db          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48


RESULT 4
US-09-865-294-71
; Sequence 71, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
;    LENGTH: 30
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-71

  Query Match             87.6%;  Score 141;  DB 10;  Length 30;
  Best Local Similarity   93.8%;  Pred. No. 2.2e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVKISITEIKGVIVHRIETILF 32
              ||||||||||  ||||||||||||||||||||
Db          1 DAEFRHDSGY--KISITEIKGVIVHRIETILF 30


RESULT 5
US-09-865-294-75
; Sequence 75, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
;    LENGTH: 34
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-75

  Query Match             84.5%;  Score 136;  DB 10;  Length 34;
  Best Local Similarity   85.3%;  Pred. No. 1.5e-13;
  Matches   29;  Conservative    2;  Mismatches    1;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEV--KISITEIKGVIVHRIETILF 32
              ||||||||||||  ||||:||||||||:|| |||
Db          1 DAEFRHDSGYEVHHKISISEIKGVIVHKIEGILF 34


RESULT 6
US-09-865-294-76
; Sequence 76, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
;    LENGTH: 34
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-76

  Query Match             80.1%;  Score 129;  DB 10;  Length 34;
  Best Local Similarity   85.3%;  Pred. No. 1.7e-12;
  Matches   29;  Conservative    1;  Mismatches    2;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEV--KISITEIKGVIVHRIETILF 32
              ||||||||||||  |||||||: ||| |||||||
Db          1 DAEFRHDSGYEVHHKISITEIRTVIVTRIETILF 34


RESULT 7
US-09-865-294-51
; Sequence 51, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
;    LENGTH: 19
;    TYPE: PRT
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;   ORGANISM: Measles virus
US-09-865-294-51

  Query Match             55.9%;  Score 90;  DB 10;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 8e-07;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 8
US-10-076-674-6
; Sequence 6, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/076,674
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-6

  Query Match             55.9%;  Score 90;  DB 14;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 9
US-10-355-161A-6
; Sequence 6, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-6

  Query Match             55.9%;  Score 90;  DB 15;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 10
US-10-076-674-11
; Sequence 11, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/076,674
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 45
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-11

  Query Match             55.9%;  Score 90;  DB 14;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 11
US-10-355-161A-11
; Sequence 11, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 45
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-11

  Query Match             55.9%;  Score 90;  DB 15;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 12
US-10-076-674-4
; Sequence 4, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
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;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/076,674
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 50
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-4

  Query Match             55.9%;  Score 90;  DB 14;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 13
US-10-355-161A-4
; Sequence 4, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 50
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-4

  Query Match             55.9%;  Score 90;  DB 15;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 14
US-10-355-161A-13
; Sequence 13, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
;   LENGTH: 65
;   TYPE: PRT
;   ORGANISM: Foot-and-mouth disease virus
US-10-355-161A-13

  Query Match             54.0%;  Score 87;  DB 15;  Length 65;
  Best Local Similarity   94.7%;  Pred. No. 1e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
              ||||||||||||:||||||
Db          1 ISITEIKGVIVHKIETILF 19


RESULT 15
US-10-355-161A-12
; Sequence 12, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 65
;   TYPE: PRT
;   ORGANISM: Foot-and-mouth disease virus
US-10-355-161A-12

  Query Match             51.6%;  Score 83;  DB 15;  Length 65;
  Best Local Similarity   89.5%;  Pred. No. 4.2e-05;
  Matches   17;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 ISITEIKGVIVHRIETILF 32
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Db          1 ISISEIKGVIVHKIETILF 19


Search completed: June 18, 2004, 20:23:47
Job time : 37.1227 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:45 ; Search time 9.61963 Seconds
(without alignments)
319.984 Million cell updates/sec

Title: US-09-865-294A-72
Perfect score: 161
Sequence: 1 DAEFRHDSGYEVKISITEIKGVIVHRIETILF 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	66	41.0	42	2	PN0512	beta-amyloid prote
2	66	41.0	57	2	E60045	Alzheimer's diseas
3	66	41.0	57	2	P60045	Alzheimer's diseas
4	66	41.0	57	2	G60045	Alzheimer's diseas
5	66	41.0	57	2	D60045	Alzheimer's diseas
6	66	41.0	57	2	A60045	Alzheimer's diseas
7	66	41.0	57	2	B60045	Alzheimer's diseas
8	66	41.0	82	2	PQ0438	Alzheimer's diseas
9	66	41.0	695	1	A49795	Alzheimer's diseas
10	66	41.0	770	1	QRHUA4	Alzheimer's diseas
11	64.5	40.1	552	2	S47034	cell fusion protei
12	64	39.8	546	1	VGNZRL	cell fusion glycop
13	61	37.9	546	2	S47300	gene F protein - r
14	60	37.3	546	1	VGNZRK	cell fusion glycop
15	60	37.3	546	2	S55386	cell fusion protei
16	60	37.3	546	2	S47305	gene F protein - r
17	59	36.6	542	2	JQ2223	cell fusion protei
18	59	36.6	662	1	VGNZCD	cell fusion glycop
19	59	36.6	662	2	S21382	cell fusion protei
20	58.5	36.3	631	1	VGNZPD	cell fusion glycop
21	58.5	36.3	631	1	A48346	cell fusion glycop
22	58	36.0	282	2	PQ0376	cell fusion glycop
23	58	36.0	282	2	PQ0388	cell fusion glycop
24	58	36.0	534	1	JU0274	cell fusion glycop
25	58	36.0	550	1	E48556	cell fusion glycop
26	58	36.0	553	1	VGNZMV	cell fusion glycop
27	57	35.4	33	2	S23094	beta-amyloid prote
28	57	35.4	220	2	T00801	probable synaptobr
29	57	35.4	229	2	F86180	hypothetical prote
30	57	35.4	695	2	A27485	Alzheimer's diseas
31	57	35.4	695	2	S00550	Alzheimer's diseas
32	55.5	34.5	219	2	D89923	endonuclease-like
33	55.5	34.5	356	2	D96537	hypothetical prote
34	53	32.9	175	2	D86180	hypothetical prote
35	53	32.9	221	2	F84741	probable synaptobr
36	53	32.9	240	2	T47589	synaptobrevin-like
37	52	32.3	1487	2	S15904	alpha-1 proteinase
38	51.5	32.0	279	2	AI1513	hypothetical prote
39	51	31.7	469	1	NIZJMN	nitrogenase (EC 1.
40	51	31.7	747	2	JH0773	Alzheimer's diseas
41	51	31.7	1451	2	B41185	alpha-2 macroglobu
42	51	31.7	1476	2	A41185	alpha-2 macroglobu
43	51	31.7	1477	2	A29952	alpha-1 proteinase
44	50	31.1	421	2	T33811	hypothetical prote
45	50	31.1	605	2	G70409	high affinity sulf

ALIGNMENTS

RESULT 1
PN0512
beta-amyloid protein - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PN0512
R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno,
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragm
A;Reference number: PN0512; MUID:93290653; PMID:7685598
A;Accession: PN0512
A;Molecule type: protein
A;Residues: 1-42 <SHI>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid

Query Match 41.0%; Score 66; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
||||||||||||
Db 1 DAEFRHDSGYEV 12

RESULT 2
E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C;Species: Ovis sp. (sheep)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: E60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: E60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56130
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 41.0%; Score 66; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
||||||||||||
Db 6 DAEFRHDSGYEV 17

RESULT 3

```
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: F60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: F60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match             41.0%;  Score 66;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db          6 DAEFRHDSGYEV 17


RESULT 4
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: G60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: G60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56126
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match             41.0%;  Score 66;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db          6 DAEFRHDSGYEV 17


RESULT 5
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: D60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: D60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56124
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match             41.0%;  Score 66;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db          6 DAEFRHDSGYEV 17


RESULT 6
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: A60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: A60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56125
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match             41.0%;  Score 66;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db          6 DAEFRHDSGYEV 17


RESULT 7
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C;Species: Ursus maritimus (polar bear)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: B60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: B60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match             41.0%;  Score 66;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db          6 DAEFRHDSGYEV 17


RESULT 8
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: PQ0438; C60045
R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A;Reference number: PQ0438; MUID:93075180; PMID:1445331
A;Accession: PQ0438
A;Molecule type: DNA
A;Residues: 1-82 <DAV>
A;Cross-references: GB:M83558; GB:M83657
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
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A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: C60045
A;Molecule type: mRNA
A;Residues: 12-68 <JOH>
A;Cross-references: EMBL:X56129
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 41.0%; Score 66; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
||||||||||||
Db 17 DAEFRHDSGYEV 28

RESULT 9
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49795
R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a p
A;Reference number: A49795; MUID:91273117; PMID:1905108
A;Accession: A49795
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-695 <POD>
A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing

Query Match 41.0%; Score 66; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
||||||||||||
Db 597 DAEFRHDSGYEV 608

RESULT 10
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibi
N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44
4668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S3
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288,'V',365-770 <LEM1>
A;Cross-references: EMBL:X13466
A;Note: alternative splice form APP(695)
R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A;Note: alternative splice form APP(695)
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prot
A;Reference number: A32277; MUID:89165870; PMID:2538123
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAP>
A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similari
A;Reference number: A33260; MUID:89392030; PMID:2675837
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM
A;Molecule type: DNA
A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duin
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorr
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheim
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 689-716,'F',718-737 <MUR>
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692,'G',694-718 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA

A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288,'V',365-770 <KAN>
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756,'S',758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344,'I',365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344,'I',365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashtc
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288,'V',365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 60
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 6
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K

  Query Match 41.0%; Score 66; DB 1; Length 770;
  Best Local Similarity 100.0%; Pred. No. 0.21;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEV 12
||||||||||||
Db 672 DAEFRHDSGYEV 683

RESULT 11
S47034
cell fusion protein precursor - porpoise morbillivirus
N;Alternate names: F protein
C;Species: porpoise morbillivirus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C;Accession: S47034
R;Bolt, G.; Gottschalck, E.; Blixenkkrone-Moeller, M.; Wishaupt, R.G.A.; Welsh, M.J.; E
submitted to the EMBL Data Library, July 1994
A;Description: Nucleotide sequence comparisons of the F and M genes of cetacean morbill
A;Reference number: S47034
A;Accession: S47034
A;Molecule type: mRNA
A;Residues: 1-552 <BOL>
A;Cross-references: EMBL:X80757; NID:g520639; PIDN:CAA56731.1; PID:g520640
A;Experimental source: isolate Ulster 88
A;Note: the source is designated as Cetacean morbillivirus
C;Superfamily: parainfluenza virus cell fusion protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-552/Product: fusion protein #status predicted <MAT>

  Query Match 40.1%; Score 64.5; DB 2; Length 552;
  Best Local Similarity 44.8%; Pred. No. 0.24;
  Matches 13; Conservative 7; Mismatches 4; Indels 5; Gaps 1;

Qy 9 GYEVKISI-----TEIKGVIVHRIETILP 32
|| : :|| :|:|||||||:| : :
Db 278 GYFIVLSIAYPTLSEVKGVIVHRLEAVSY 306

RESULT 12
VGNZRL

```
cell fusion glycoprotein precursor - rinderpest virus (strain L)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: rinderpest virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Accession: A28921
R;Tsukiyama, K.; Yoshikawa, Y.; Yamanouchi, K.
Virology 164, 523-530, 1988
A;Title: Fusion glycoprotein (F) of rinderpest virus: entire nucleotide sequence of the
A;Reference number: A28921; MUID:88219541; PMID:3285575
A;Accession: A28921
A;Molecule type: mRNA
A;Residues: 1-546 <TSU>
A;Cross-references: GB:M20870; NID:g333898; PIDN:AAA47399.1; PID:g333899
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-104/Product: cell fusion glycoprotein F2 #status predicted <FG2>
F;105-546/Product: cell fusion glycoprotein F1 #status predicted <FG1>
F;109-133/Domain: transmembrane #status predicted <TN1>
F;485-513/Domain: transmembrane #status predicted <TN2>
F;25,57,63/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             39.8%;  Score 64;  DB 1;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 0.28;
  Matches   11;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         15 SITEIKGVIVHRIETILF 32
              |::|||||||||:|:: :
Db        283 SLSEIKGVIVHRLESVSY 300


RESULT 13
S47300
gene F protein - rinderpest virus
C;Species: rinderpest virus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Oct-1999
C;Accession: S47300; PQ0865
R;Evans, S.A.; Baron, M.D.; Chamberlain, R.W.; Goatley, L.; Barrett, T.
submitted to the EMBL Data Library, March 1994
A;Description: The complete nucleotide sequence of the fusion protein gene of the vaccin
A;Reference number: S47299
A;Accession: S47300
A;Molecule type: DNA
A;Residues: 1-546 <EVA>
A;Cross-references: EMBL:Z31656; NID:g535406; PIDN:CAA83482.1; PID:g535407
R;Chamberlain, R.W.; Wamwayi, H.M.; Hockley, E.; Shaila, M.S.; Goatley, L.; Knowles, N.J
J. Gen. Virol. 74, 2775-2780, 1993
A;Title: Evidence for different lineages of rinderpest virus reflecting their geographic
A;Reference number: PQ0865; MUID:94103786; PMID:8277286
A;Accession: PQ0865
A;Molecule type: mRNA
A;Residues: 86-191 <CHA>
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein

  Query Match             37.9%;  Score 61;  DB 2;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 0.77;
  Matches   11;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         15 SITEIKGVIVHRIETILF 32
              |::|||||||||:| : :
Db        283 SLSEIKGVIVHRLEGVSY 300


RESULT 14
VGNZRK
cell fusion glycoprotein precursor - rinderpest virus (strain Kabete O)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: rinderpest virus
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 25-Oct-1996
C;Accession: A31051
R;Hsu, D.; Yamanaka, M.; Miller, J.; Dale, B.; Grubman, M.; Yilma, T.
Virology 166, 149-153, 1988
A;Title: Cloning of the fusion gene of rinderpest virus: comparative sequence analysis
A;Reference number: A31051; MUID:88322864; PMID:3413983
A;Accession: A31051
A;Molecule type: genomic RNA
A;Residues: 1-546 <HSU>
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-108/Product: cell fusion glycoprotein F2 #status predicted <FF1>
F;109-546/Product: cell fusion glycoprotein F1 #status predicted <FF2>
F;109-134/Domain: transmembrane #status predicted <TN1>
F;491-513/Domain: transmembrane #status predicted <TN2>
F;25,57,63,518/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             37.3%;  Score 60;  DB 1;  Length 546;
  Best Local Similarity   55.6%;  Pred. No. 1.1;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         15 SITEIKGVIVHRIETILF 32
              |::|||||||:||:| : :
Db        283 SLSEIKGVIIHRLEGVSY 300


RESULT 15
S55386
cell fusion protein - peste-des-petits-ruminants virus (strain 75/1)
N;Alternate names: F protein
C;Species: peste-des-petits-ruminants virus
A;Variety: strain 75/1
C;Date: 23-May-1997 #sequence_revision 23-May-1997 #text_change 20-Sep-1999
C;Accession: S55386
R;Meyer, G.; Diallo, A.
submitted to the EMBL Data Library, September 1994
A;Description: The nucleotide sequence of fusion protein gene of the Peste des petits r
to each virus.
A;Reference number: S55386
A;Accession: S55386
A;Molecule type: DNA
A;Residues: 1-546 <MEY>
A;Cross-references: EMBL:Z37017; NID:g854372; PIDN:CAA85451.1; PID:g854373
A;Experimental source: strain 75/1; cell line vero
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: membrane fusion

  Query Match             37.3%;  Score 60;  DB 2;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 1.1;
  Matches   11;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         15 SITEIKGVIVHRIETILF 32
              :::|||||||||:|| | :
Db        283 TLSEIKGVIVHKIEAISY 300


Search completed: June 18, 2004, 20:03:30
Job time : 9.61963 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:55 ; Search time 6.28221 Seconds
(without alignments)
265.232 Million cell updates/sec

Title: US-09-865-294A-72
Perfect score: 161
Sequence: 1 DAEFRHDSGYEVKISITEIKGVIVHRIETILF 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	66	41.0	57	1	A4_URSMA	Q29149 ursus marit
2	66	41.0	58	1	A4_CANFA	Q28280 canis famil
3	66	41.0	58	1	A4_RABIT	Q28748 oryctolagus
4	66	41.0	58	1	A4_SHEEP	Q28757 ovis aries
5	66	41.0	59	1	A4_BOVIN	Q28053 bos taurus
6	66	41.0	751	1	A4_SAISC	Q95241 s amyloid b
7	66	41.0	770	1	A4_CAVPO	Q60495 c amyloid b
8	66	41.0	770	1	A4_HUMAN	P05067 h amyloid b
9	66	41.0	770	1	A4_MACFA	P53601 m amyloid b
10	66	41.0	770	1	A4_PIG	P79307 s amyloid b
11	64	39.8	546	1	VGLF_RINDL	P10864 rinderpest
12	61	37.9	546	1	VGLF_RINDB	P41360 rinderpest
13	60	37.3	546	1	VGLF_RINDR	P41356 rinderpest
14	59	36.6	662	1	VGLF_CDVO	P12569 canine dist
15	58.5	36.3	631	1	VGLF_PHODV	P28886 phocine dis
16	58	36.0	534	1	VGLF_MEASY	P26032 measles vir
17	58	36.0	550	1	VGLF_MEASA	P35973 measles vir
18	58	36.0	550	1	VGLF_MEASE	P08300 measles vir
19	57	35.4	220	1	V725_ARATH	O48850 arabidopsis
20	57	35.4	229	1	V726_ARATH	Q9mas5 arabidopsis
21	57	35.4	770	1	A4_MOUSE	P12023 m amyloid b
22	57	35.4	770	1	A4_RAT	P08592 r amyloid b
23	55.5	34.5	356	1	BCA6_ARATH	Q9lpm9 arabidopsis
24	54	33.5	546	1	VGLF_RINDK	P12574 rinderpest
25	53	32.9	219	1	V721_ARATH	Q9ztw3 arabidopsis
26	53	32.9	221	1	V722_ARATH	P47192 arabidopsis
27	53	32.9	240	1	V727_ARATH	Q9m376 arabidopsis
28	51	31.7	469	1	NIFN_BRAJA	P26507 bradyrhizob
29	51	31.7	1451	1	A2M2_MOUSE	P28666 mus musculu
30	51	31.7	1476	1	A2M1_MOUSE	P28665 mus musculu
31	51	31.7	1477	1	A1I3_RAT	P14046 rattus norv
32	50	31.1	506	1	MATK_RHOFR	O62984 rhododendro
33	50	31.1	529	1	VGLF_MEASI	P26031 measles vir
34	49	30.4	244	1	YSCJ_YEREN	Q01251 yersinia en
35	49	30.4	244	1	YSCJ_YERPE	Q00926 yersinia pe
36	49	30.4	481	1	GATB_FUSNN	Q8r680 fusobacteri
37	49	30.4	506	1	MATK_RHOTS	O62991 rhododendro
38	48	29.8	254	1	PMG3_HUMAN	Q8n0y7 homo sapien
39	48	29.8	254	1	PMG3_PANTR	Q8mke8 pan troglod
40	48	29.8	316	1	YMX1_CAEEL	P34509 caenorhabdi
41	48	29.8	384	1	Y955_SYNY3	P74328 synechocyst
42	47.5	29.5	367	1	BCA7_ARATH	Q9lpm8 arabidopsis
43	47	29.2	711	1	LXE3_HUMAN	Q9byj1 homo sapien
44	46.5	28.9	181	1	YB33_ARCFU	O28839 archaeoglob
45	46.5	28.9	196	1	GCH2_YERPE	Q8zef0 yersinia pe

ALIGNMENTS

RESULT 1
A4_URSMA
ID A4_URSMA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ursus maritimus (Polar bear) (Thalarctos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC --

CC --
DR EMBL; X56128; CAA39593.1; -.
DR PIR; B60045; B60045.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 41.0%; Score 66; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db          6 DAEFRHDSGYEV 17


RESULT 2
A4_CANFA
ID   A4_CANFA       STANDARD;      PRT;    58 AA.
AC   Q28280;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56125; CAA39590.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     58       POTENTIAL.
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6285 MW;  8469D488A2E12DFA CRC64;

  Query Match             41.0%;  Score 66;  DB 1;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.0047;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db          7 DAEFRHDSGYEV 18


RESULT 3
A4_RABIT
ID   A4_RABIT       STANDARD;      PRT;    58 AA.
AC   Q28748;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56129; CAA39594.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   DOMAIN       58    >58       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6300 MW;  F434209D88EBA82D CRC64;

  Query Match             41.0%;  Score 66;  DB 1;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.0047;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db          6 DAEFRHDSGYEV 17


RESULT 4
A4_SHEEP
ID   A4_SHEEP       STANDARD;      PRT;    58 AA.
AC   Q28757;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
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RC   TISSUE=Heart;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56130; CAA39595.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   DOMAIN       58    >58       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6300 MW;  F434209D88EBA82D CRC64;

  Query Match             41.0%;  Score 66;  DB 1;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.0047;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db          6 DAEFRHDSGYEV 17


RESULT 5
A4_BOVIN
ID   A4_BOVIN       STANDARD;      PRT;    59 AA.
AC   Q28053;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56124; CAA39589.1; -.
DR   EMBL; X56126; CAA39591.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     58       POTENTIAL.
FT   DOMAIN       59    >59       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      59     59
SQ   SEQUENCE   59 AA;  6414 MW;  F43469D488A2E12D CRC64;

  Query Match             41.0%;  Score 66;  DB 1;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 0.0048;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db          7 DAEFRHDSGYEV 18


RESULT 6
A4_SAISC
ID   A4_SAISC       STANDARD;      PRT;    751 AA.
AC   Q95241;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
DE   APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
DE   Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
DE   CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Liver;
RX   MEDLINE=96108492; PubMed=8532114;
RA   Levy E., Amorim A., Frangione B., Walker L.C.;
RT   "Beta-amyloid precursor protein gene in squirrel monkeys with
RT   cerebral amyloid angiopathy.";
RL   Neurobiol. Aging 16:805-808(1995).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(0) alpha ATPase activity (By similarity).
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CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=Q95241-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q95241-2; Sequence=Not described;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; S81024; AAD14347.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Amyloid; Alternative splicing.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    751       A4 PROTEIN.
FT   CHAIN        18    668       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    652       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       653    751       C99 (POTENTIAL).
FT   CHAIN       653    694       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN       653    692       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN       669    751       C83 (POTENTIAL).
FT   CHAIN       669    694       P3(42) (POTENTIAL).
FT   CHAIN       669    692       P3(40) (POTENTIAL).
FT   CHAIN       693    751       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN       695    751       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN       702    751       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN       721    751       C31 (POTENTIAL).
FT   DOMAIN       18    680       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    681    704       POTENTIAL.
FT   DOMAIN      705    751       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      316    344       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      363    428       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      504    521       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      713    732       INTERACTION WITH G(O)-ALPHA
FT                                (BY SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND.
FT   SITE        652    653       CLEAVAGE (BY BETA-SECRETASE)
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FT                                     (BY SIMILARITY).
FT   SITE        653    654        CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        668    669        CLEAVAGE (BY ALPHA-SECRETASE)
FT                                     (BY SIMILARITY).
FT   SITE        685    685        INVOLVED IN FREE RADICAL PROPAGATION
FT                                     (BY SIMILARITY).
FT   SITE        687    687        INVOLVED IN OXIDATIVE REACTIONS
FT                                     (BY SIMILARITY).
FT   SITE        692    693        CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                     (BY SIMILARITY).
FT   SITE        694    695        CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                     (BY SIMILARITY).
FT   SITE        701    702        CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                     (BY SIMILARITY).
FT   SITE        705    715        BASOLATERAL SORTING SIGNAL
FT                                     (BY SIMILARITY).
FT   SITE        720    721        CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT                                     (BY SIMILARITY).
FT   SITE        738    741        ENDOCYTOSIS SIGNAL.
FT   SITE        740    743        NPXY MOTIF.

  Query Match             41.0%;  Score 66;  DB 1;  Length 751;
  Best Local Similarity   100.0%;  Pred. No. 0.071;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db        653 DAEFRHDSGYEV 664


RESULT 7
A4_CAVPO
ID   A4_CAVPO       STANDARD;      PRT;   770 AA.
AC   Q60495; Q60496;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
DE   protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
DE   P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE   CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
GN   APP.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Liver;
RX   MEDLINE=97236426; PubMed=9116031;
RA   Beck M., Mueller D., Bigl V.;
RT   "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT   alternative splicing.";
RL   Biochim. Biophys. Acta 1351:17-21(1997).
RN   [2]
RP   INTERACTION OF BETA-APP40 WITH APOE.
RX   MEDLINE=98007700; PubMed=9349544;
RA   Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
RA   Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
RT   "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
RT   cerebral capillary sequestration and blood-brain barrier transport of
RT   circulating Alzheimer's amyloid beta.";
RL   J. Neurochem. 69:1995-2004(1997).
RN   [3]
RP   PROCESSING.
RX   MEDLINE=20084499; PubMed=10619481;
RA   Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA   Bigl V.;
RT   "Guinea-pig primary cell cultures provide a model to study expression
RT   and amyloidogenic processing of endogenous amyloid precursor
RT   protein.";
RL   Neuroscience 95:243-254(2000).
RN   [4]
RP   GAMMA-SECRETASE PROCESSING.
RX   MEDLINE=20576391; PubMed=11035007;
RA   Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA   Ziani-Cherif C., Onstead L., Sambamurti K.;
RT   "A novel gamma -secretase assay based on detection of the putative
RT   C-terminal fragment-gamma of amyloid beta protein precursor.";
RL   J. Biol. Chem. 276:481-487(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC       and apoliproteins E and J in the CSF and to HDL particles in
CC       plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) and DDB1 (By similarity).
CC       Associates with microtubules in the presence of ATP and in a
CC       kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC       all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC       ApoE3 appears to be the preferred amyloid binding isoform, while
CC       the apoE4 isoform-beta-APP40 complex is capable of being
CC       transported across the blood-brain barrier.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated pits
CC       (By similarity). During maturation, the immature APP (N-
CC       glycosylated in the endoplasmic reticulum) moves to the Golgi
CC       complex where complete maturation occurs (O-glycosylated and
CC       sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC       APP is released into the extracellular space and the C-terminal is
CC       internalized to endosomes and lysosomes (By similarity). Some APP
CC       accumulates in secretory transport vesicles leaving the late Golgi
CC       compartment and returns to the cell surface (By similarity). APP
CC       sorts to the basolateral surface in epithelial cells (By
CC       similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms, missing exons 7,8 and 15, seem to
CC         exist. The L-isoforms, missing exon 15, are referred to as
CC         appicans;
CC       Name=APP770;
CC         IsoId=Q60495-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
CC   -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC       brain. The longer isoforms containing the BPTI domain are
```

```
CC       predominantly expressed in peripheral organs such as muscle and
CC       liver.
CC   -!- INDUCTION: Increased levels during neuronal differentiation.
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells.
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue (By similarity). The NPXY site is also involved in
CC       clathrin-mediated endocytosis.
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC       gamma-secretase yields P3 peptides. This is the major secretory
CC       pathway and is nonamyloidogenic. Alternatively,
CC       presenilin/nicastrin-mediated gamma-secretase processing of CTF-
CC       beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC       and amyloid-beta 42 (Abeta42), major components of amyloid
CC       plaques, and the corresponding cytotoxic C-terminal fragments
CC       (CTFs).
CC   -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC       apoptosis (By similarity).
CC   -!- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
CC       the L-APP isoforms produces the APP proteoglycan core proteins,
CC       the appicans (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific (By similarity).
CC       Phosphorylation can affect APP processing, neuronal
CC       differentiation and interaction with other proteins.
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X97631; CAA66230.1; -.
DR   EMBL; X99198; CAA67589.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (BY SIMILARITY).
FT   CHAIN        18    671       SOLUBLE APP-BETA (BY SIMILARITY).
FT   CHAIN       672    770       CTF-ALPHA (BY SIMILARITY).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688    770       CTF-BETA (BY SIMILARITY).
FT   CHAIN       688    713       P3(42) (BY SIMILARITY).
FT   CHAIN       688    711       P3(40) (BY SIMILARITY).
FT   CHAIN       712    770       GAMMA-CTF(59) (BY SIMILARITY).
FT   CHAIN       714    770       GAMMA-CTF(57) (BY SIMILARITY).

  Query Match             41.0%;  Score 66;  DB 1;  Length 770;
  Best Local Similarity   100.0%;  Pred. No. 0.073;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db        672 DAEFRHDSGYEV 683


RESULT 8
A4_HUMAN
ID   A4_HUMAN       STANDARD;      PRT;   770 AA.
AC   P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
AC   Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCC8; Q9UCD1; Q9UQ58;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE   nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE   alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE   (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE   P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE   (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE   secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE   (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE   (Amyloid intracellular domain 50) (AID(50)); C31].
GN   APP OR A4 OR AD1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=87144572; PubMed=2881207;
RA   Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA   Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT   "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT   cell-surface receptor.";
RL   Nature 325:733-736(1987).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM APP751).
RC   TISSUE=Brain;
RX   MEDLINE=88122639; PubMed=2893289;
RA   Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA   Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA   Cordell B.;
RT   "A new A4 amyloid mRNA contains a domain homologous to serine
RT   proteinase inhibitors.";
RL   Nature 331:525-527(1988).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RX   MEDLINE=89128427; PubMed=2783775;
RA   Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA   Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT   "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT   is encoded by 16 exons.";
RL   Nucleic Acids Res. 17:517-522(1989).
```

RN [4]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";
RL Gene 87:257-263(1990).
RN [5]
RP ERRATUM, AND REVISIONS.
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RL Gene 102:291-292(1991).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
RC TISSUE=Leukocyte;
RX MEDLINE=92268136; PubMed=1587857;
RA Koenig G., Moenning U., Czech C., Prior R., Banati R.,
RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
RT "Identification and differential expression of a novel alternative
RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
RT leukocytes and brain microglial cells.";
RL J. Biol. Chem. 267:10804-10809(1992).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM APP639).
RC TISSUE=Brain;
RX MEDLINE=22744650; PubMed=12859342;
RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
RT "Identification of a novel alternative splicing isoform of human
RT amyloid precursor protein gene, APP639.";
RL Eur. J. Neurosci. 18:102-108(2003).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM APP305).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [11]
RP ERRATUM, AND REVISIONS.
RA Mita S., Sadlock J., Herbert J., Schon E.A.;
RL Nucleic Acids Res. 16:11402-11402(1988).
RN [12]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE=89165870; PubMed=2538123;
RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
RT "Characterization of the 5'-end region and the first two exons of the
RT beta-protein precursor gene.";
RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
RN [13]
RP SEQUENCE OF 18-50.
RC TISSUE=Fibroblast;
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [14]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=89346754; PubMed=2569763;
RA de Sauvage F., Octave J.N.;
RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT secreted protein.";
RL Science 245:651-653(1989).
RN [15]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [16]
RP SEQUENCE OF 286-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [17]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [18]
RP SEQUENCE OF 507-770 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [19]
RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX MEDLINE=96139497; PubMed=8576160;
RA Beher D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [20]
RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717
RP AND AD GLY-717.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzcwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
RN [21]
RP SEQUENCE OF 656-737 FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;

```
RA   Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA   Little S.P.;
RT   "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT   similarity to soybean trypsin inhibitor.";
RL   Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN   [22]

  Query Match             41.0%;  Score 66;  DB 1;  Length 770;
  Best Local Similarity   100.0%;  Pred. No. 0.073;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db        672 DAEFRHDSGYEV 683


RESULT 9
A4_MACFA
ID   A4_MACFA       STANDARD;      PRT;   770 AA.
AC   P53601; Q95KN7;
DT   01-OCT-1996 (Rel. 34, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC   TISSUE=Cerebellum;
RX   MEDLINE=91273117; PubMed=1905108;
RA   Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT   "Homology of the amyloid beta protein precursor in monkey and human
RT   supports a primate model for beta amyloidosis in Alzheimer's
RT   disease.";
RL   Am. J. Pathol. 138:1423-1435(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=P53601-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
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CC   ----------------------------------------------------------------------
DR   EMBL; M58727; AAA36829.1; -.
DR   EMBL; M58726; AAA36828.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672    770       C99 (POTENTIAL).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN       688    770       C83 (POTENTIAL).
FT   CHAIN       688    713       P3(42) (POTENTIAL).
FT   CHAIN       688    711       P3(40) (POTENTIAL).
FT   CHAIN       712    770       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN       714    770       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN       721    770       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN       740    770       C31 (POTENTIAL).
FT   DOMAIN       18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    700    723       POTENTIAL.
FT   DOMAIN      724    770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      391    423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      491    522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      523    540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      732    751       INTERACTION WITH G(O)-ALPHA
FT                                (BY SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND (BY SIMILARITY).
FT   SITE        671    672       CLEAVAGE (BY BETA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        672    673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        687    688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        704    704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                                (BY SIMILARITY).
FT   SITE        706    706       INVOLVED IN OXIDATIVE REACTIONS
FT                                (BY SIMILARITY).
FT   SITE        711    712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                (BY SIMILARITY).
FT   SITE        713    714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                (BY SIMILARITY).
FT   SITE        720    721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                (BY SIMILARITY).
FT   SITE        724    734       BASOLATERAL SORTING SIGNAL
FT                                (BY SIMILARITY).
FT   SITE        739    740       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
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  Query Match           41.0%;  Score 66;  DB 1;  Length 770;
  Best Local Similarity  100.0%;  Pred. No. 0.073;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db        672 DAEFRHDSGYEV 683


RESULT 10
A4_PIG
ID   A4_PIG          STANDARD;      PRT;   770 AA.
AC   P79307; Q29023; Q9TUI0;
DT   01-NOV-1997 (Rel. 35, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura A., Takahashi T.;
RT   "Amyloid precursor protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-136 FROM N.A.
RC   TISSUE=Small intestine;
RA   Winteroe A.K., Fredholm M.;
RT   "Evaluation and characterization of a porcine small intestine cDNA
RT   library.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 667-723 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
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CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB032550; BAA84580.1; -.
DR   EMBL; Z84022; CAB06313.1; -.
DR   EMBL; X56127; CAA39592.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Amyloid.
FT   SIGNAL        1    17       BY SIMILARITY.
FT   CHAIN        18   770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18   687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18   671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672   770       C99 (BY SIMILARITY).
FT   CHAIN       672   713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672   711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688   770       C83 (BY SIMILARITY).
FT   CHAIN       688   713       P3(42) (BY SIMILARITY).
FT   CHAIN       688   711       P3(40) (BY SIMILARITY).
FT   CHAIN       712   770       GAMMA-CTF(59).
FT   CHAIN       714   770       GAMMA-CTF(57).
FT   CHAIN       721   770       GAMMA-CTF(50) (BY SIMILARITY).
FT   CHAIN       740   770       C31 (DURING APOPTOSIS) (BY SIMILARITY).
FT   DOMAIN       18   699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    700   723       POTENTIAL.
FT   DOMAIN      724   770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96   110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      135   155       COPPER-BINDING (BY SIMILARITY).
FT   DOMAIN      181   188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291   341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      391   423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      491   522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      523   540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      732   751       INTERACTION WITH G(O)-ALPHA (BY
FT                               SIMILARITY).
FT   DOMAIN      230   260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274   280       POLY-THR.
FT   SITE        144   144       REQUIRED FOR COPPER(II) REDUCTION
FT                               (BY SIMILARITY).
FT   ACT_SITE    301   302       REACTIVE BOND (BY SIMILARITY).
FT   SITE        671   672       CLEAVAGE (BY BETA-SECRETASE)
FT                               (BY SIMILARITY).
FT   SITE        672   673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        687   688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                               (BY SIMILARITY).
FT   SITE        704   704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                               (BY SIMILARITY).
FT   SITE        706   706       INVOLVED IN OXIDATIVE REACTIONS
FT                               (BY SIMILARITY).
FT   SITE        711   712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                               (BY SIMILARITY).
FT   SITE        713   714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                               (BY SIMILARITY).
FT   SITE        720   721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)

  Query Match             41.0%;  Score 66;  DB 1;  Length 770;
  Best Local Similarity   100.0%;  Pred. No. 0.073;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db        672 DAEFRHDSGYEV 683
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RESULT 11
VGLF_RINDL
ID   VGLF_RINDL     STANDARD;      PRT;   546 AA.
AC   P10864;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Rinderpest virus (strain L) (RDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11243;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88219541; PubMed=3285575;
RA   Tsukiyama K., Yoshikawa Y., Yamanouchi K.;
RT   "Fusion glycoprotein (F) of rinderpest virus: entire nucleotide
RT   sequence of the F mRNA, and several features of the F protein.";
RL   Virology 164:523-530(1988).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M20870; AAA47399.1; -.
DR   PIR; A28921; VGNZRL.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    546       FUSION GLYCOPROTEIN F0.
FT   CHAIN        20    108       F2 PROTEIN.
FT   CHAIN       109    546       F1 PROTEIN.
FT   DOMAIN      104    108       ARG/LYS-RICH (BASIC).
FT   TRANSMEM    109    133       POTENTIAL.
FT   TRANSMEM    484    513       POTENTIAL.
FT   DOMAIN      514    517       ARG/LYS-RICH (BASIC).
FT   DISULFID     64    191       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD     25     25       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     57     57       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     63     63       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   546 AA;  58911 MW;  985029418F28FFB5 CRC64;

  Query Match             39.8%;  Score 64;  DB 1;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 0.1;
  Matches   11;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         15 SITEIKGVIVHRIETILF 32
              |::|||||||||:|:: :
Db        283 SLSEIKGVIVHRLESVSY 300


RESULT 12
VGLF_RINDB
ID   VGLF_RINDB     STANDARD;      PRT;   546 AA.
AC   P41360;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Rinderpest virus (strain RBT1) (RDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=39007;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95088609; PubMed=7996154;
RA   Evans S.A., Baron M.D., Chamberlain R.W., Goatley L., Barrett T.;
RT   "Nucleotide sequence comparisons of the fusion protein gene from
RT   virulent and attenuated strains of rinderpest virus.";
RL   J. Gen. Virol. 75:3611-3617(1994).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z31656; CAA83482.1; -.
DR   PIR; S47300; S47300.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    546       FUSION GLYCOPROTEIN F0.
FT   CHAIN        20    108       F2 PROTEIN.
FT   CHAIN       109    546       F1 PROTEIN.
FT   DOMAIN      104    108       ARG/LYS-RICH (BASIC).
FT   TRANSMEM    109    133       POTENTIAL.
FT   TRANSMEM    484    513       POTENTIAL.
FT   DOMAIN      514    517       ARG/LYS-RICH (BASIC).
FT   DISULFID     64    191       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD     25     25       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     57     57       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     63     63       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    518    518       O-LINKED (POTENTIAL).
SQ   SEQUENCE   546 AA;  58418 MW;  38B539B89344F401 CRC64;

  Query Match             37.9%;  Score 61;  DB 1;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 0.28;
  Matches   11;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         15 SITEIKGVIVHRIETILF 32
              |::|||||||||:| : :
Db        283 SLSEIKGVIVHRLEGVSY 300


RESULT 13
VGLF_RINDR
ID   VGLF_RINDR     STANDARD;      PRT;   546 AA.
AC   P41356;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Rinderpest virus (strain RBOK) (RDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
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OX   NCBI_TaxID=36409;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95088609; PubMed=7996154;
RA   Evans S.A., Baron M.D., Chamberlain R.W., Goatley L., Barrett T.;
RT   "Nucleotide sequence comparisons of the fusion protein gene from
RT   virulent and attenuated strains of rinderpest virus.";
RL   J. Gen. Virol. 75:3611-3617(1994).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z30700; CAA83186.1; -.
DR   EMBL; Z30697; CAA83181.1; -.
DR   PIR; S47305; S47305.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    546       FUSION GLYCOPROTEIN F0.
FT   CHAIN        20    108       F2 PROTEIN.
FT   CHAIN       109    546       F1 PROTEIN.
FT   DOMAIN      104    108       ARG/LYS-RICH (BASIC).
FT   TRANSMEM    109    133       POTENTIAL.
FT   TRANSMEM    484    513       POTENTIAL.
FT   DOMAIN      514    517       ARG/LYS-RICH (BASIC).
FT   DISULFID     64    191       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD     25     25       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     57     57       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     63     63       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    518    518       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   546 AA;  58705 MW;  ED3DF8AFFDBECB95 CRC64;

  Query Match             37.3%;  Score 60;  DB 1;  Length 546;
  Best Local Similarity   55.6%;  Pred. No. 0.4;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         15 SITEIKGVIVHRIETILF 32
              |::||||||:||:| : :
Db        283 SLSEIKGVIIHRLEGVSY 300


RESULT 14
VGLF_CDVO
ID   VGLF_CDVO      STANDARD;      PRT;   662 AA.
AC   P12569; Q65991;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Canine distemper virus (strain Onderstepoort) (CDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11233;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88129050; PubMed=3433924;
RA   Barrett T., Clarke D.K., Evans S.A., Rima B.K.;
RT   "The nucleotide sequence of the gene encoding the F protein of canine
RT   distemper virus: a comparison of the deduced amino acid sequence with
RT   other paramyxoviruses.";
RL   Virus Res. 8:373-386(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93227696; PubMed=8470428;
RA   Wild T.F., Bernard A., Spehner D., Villeval D., Drillien R.;
RT   "Vaccination of mice against canine distemper virus-induced
RT   encephalitis with vaccinia virus recombinants encoding measles or
RT   canine distemper virus antigens.";
RL   Vaccine 11:438-444(1993).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M21849; AAA42878.1; -.
DR   EMBL; X65509; CAA46481.1; -.
DR   PIR; JS0321; VGNZCD.
DR   PIR; S21382; S21382.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL        1      ?
FT   CHAIN         ?    662       FUSION GLYCOPROTEIN F0.
FT   CHAIN         ?    224       PROTEIN F2.
FT   CHAIN       225    662       PROTEIN F1.
FT   TRANSMEM    606    629       POTENTIAL.
FT   DISULFID    180    307       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT      3      3       R -> K (IN REF. 2).
FT   CONFLICT    140    140       D -> N (IN REF. 2).
FT   CONFLICT    152    152       N -> S (IN REF. 2).
FT   CONFLICT    171    171       I -> M (IN REF. 2).
FT   CONFLICT    174    174       A -> V (IN REF. 2).
FT   CONFLICT    662    662       L -> H (IN REF. 2).
SQ   SEQUENCE   662 AA;  72970 MW;  FB2C81C9797805F0 CRC64;

  Query Match             36.6%;  Score 59;  DB 1;  Length 662;
  Best Local Similarity   50.0%;  Pred. No. 0.68;
  Matches    9;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         15 SITEIKGVIVHRIETILF 32
              :::|:|||||||:| : :
Db        399 TLSEVKGVIVHRLEAVSY 416


RESULT 15
VGLF_PHODV
ID   VGLF_PHODV     STANDARD;      PRT;   631 AA.
AC   P28886;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Phocine distemper virus (PDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
```

```
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11240;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Isolate DK88-4A;
RX   MEDLINE=92113538; PubMed=1765768;
RA   Koevamees J., Blixenkrone-Moeller M., Sharma B., Oervell C.,
RA   Norrby E.;
RT   "The nucleotide sequence and deduced amino acid composition of the
RT   haemagglutinin and fusion proteins of the morbillivirus phocid
RT   distemper virus.";
RL   J. Gen. Virol. 72:2959-2966(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Ulster/88;
RX   MEDLINE=92398437; PubMed=1524494;
RA   Curran M.D., Lu Y.J., Rima B.K.;
RT   "The fusion protein gene of phocine distemper virus: nucleotide and
RT   deduced amino acid sequences and a comparison of morbillivirus fusion
RT   proteins.";
RL   Arch. Virol. 126:159-169(1992).
RN   [3]
RP   SEQUENCE OF 95-631 FROM N.A.
RC   STRAIN=Ulster/88;
RX   MEDLINE=91089508; PubMed=2264246;
RA   Curran M.D., Loan D.O., Rima B.K., Kennedy S.;
RT   "Nucleotide sequence analysis of phocine distemper virus reveals its
RT   distinctness from canine distemper virus.";
RL   Vet. Rec. 127:430-431(1990).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D10371; BAA01206.1; -.
DR   PIR; A48346; A48346.
DR   PIR; JQ1368; VGNZPD.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL        1      ?
FT   CHAIN         ?    631       FUSION GLYCOPROTEIN F0.
FT   CHAIN         ?    188       F2 PROTEIN.
FT   CHAIN       194    631       F1 PROTEIN.
FT   DISULFID    149    276       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   TRANSMEM     89    106       POTENTIAL.
FT   TRANSMEM    194    212       POTENTIAL.
FT   TRANSMEM    575    595       POTENTIAL.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    142    142       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    148    148       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     63     63       I -> V (IN REF. 2).
SQ   SEQUENCE   631 AA;  68873 MW;  D1FC87CDD426E9B8 CRC64;

  Query Match             36.3%;  Score 58.5;  DB 1;  Length 631;
  Best Local Similarity   40.0%;  Pred. No. 0.77;
  Matches   12;  Conservative    8;  Mismatches    5;  Indels    5;  Gaps    1;

Qy          8 SGYEVKISI-----TEIKGVIVHRIETILF 32
              ||  : :||     :|:|||:|||:| : :
Db        356 SGKFIVLSISYPTLSEVKGVVVHRLEAVSY 385
```

Search completed: June 18, 2004, 19:59:37
Job time : 7.28221 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:15 ; Search time 31.0184 Seconds
(without alignments)
325.503 Million cell updates/sec

Title: US-09-865-294A-72
Perfect score: 161
Sequence: 1 DAEFRHDSGYEVKISITEIKGVIVHRIETILF 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	67	41.6	82	4	Q16014	Q16014 homo sapien
2	66	41.0	19	4	Q9UCC8	Q9ucc8 homo sapien
3	66	41.0	28	4	Q9UCD1	Q9ucd1 homo sapien
4	66	41.0	30	4	Q9UCA9	Q9uca9 homo sapien
5	66	41.0	33	4	Q9UC33	Q9uc33 homo sapien
6	66	41.0	82	4	Q16020	Q16020 homo sapien
7	66	41.0	82	4	Q16019	Q16019 homo sapien
8	66	41.0	113	13	Q8JH58	Q8jh58 chelydra se
9	66	41.0	534	13	O93296	O93296 gallus gall
10	66	41.0	569	13	Q9PVL1	Q9pvl1 gallus gall
11	66	41.0	695	13	Q9DGJ8	Q9dgj8 gallus gall
12	66	41.0	751	13	Q9DGJ7	Q9dgj7 gallus gall
13	64.5	40.1	552	12	Q66147	Q66147 cetacean mo
14	61.5	38.2	552	12	Q66409	Q66409 dolphin mor
15	61.5	38.2	552	12	O56852	O56852 dolphin mor
16	61	37.9	35	4	Q8WZ99	Q8wz99 homo sapien
17	61	37.9	546	12	Q91HA5	Q91ha5 rinderpest
18	60	37.3	546	12	Q84926	Q84926 peste-des-p
19	59	36.6	528	12	Q9YJW9	Q9yjw9 canine dist
20	59	36.6	530	12	Q8QV06	Q8qv06 canine dist
21	59	36.6	662	12	Q9DXZ2	Q9dxz2 canine dist
22	59	36.6	662	12	Q91KN3	Q91kn3 canine dist
23	59	36.6	662	12	Q9YKL7	Q9ykl7 canine dist
24	59	36.6	662	12	O89327	O89327 canine dist
25	58	36.0	534	12	Q04243	Q04243 measles vir
26	58	36.0	537	12	Q04242	Q04242 measles vir
27	58	36.0	545	12	Q9PXA4	Q9pxa4 measles vir
28	58	36.0	550	12	P90331	P90331 measles vir
29	58	36.0	550	12	Q9QEX0	Q9qex0 measles vir
30	58	36.0	550	12	Q9QEW9	Q9qew9 measles vir
31	58	36.0	550	12	P90330	P90330 measles vir
32	58	36.0	550	12	Q9QEW7	Q9qew7 measles vir
33	58	36.0	550	12	Q9WMK4	Q9wmk4 measles vir
34	58	36.0	550	12	Q89495	Q89495 measles vir
35	58	36.0	550	12	Q8V049	Q8v049 measles vir
36	58	36.0	550	12	Q9YJ94	Q9yj94 measles vir
37	58	36.0	550	12	Q9QEX1	Q9qex1 measles vir
38	58	36.0	550	12	Q9QEW8	Q9qew8 measles vir
39	58	36.0	553	12	O93055	O93055 measles vir
40	58	36.0	553	12	Q9IC36	Q9ic36 measles vir
41	58	36.0	553	12	P88973	P88973 measles vir
42	58	36.0	553	12	Q83536	Q83536 measles vir
43	58	36.0	553	12	O11383	O11383 measles vir
44	58	36.0	553	12	Q9IFK2	Q9ifk2 measles vir
45	58	36.0	553	12	Q83533	Q83533 measles vir

ALIGNMENTS

RESULT 1
Q16014
ID Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzcwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26263.2; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 41.6%; Score 67; DB 4; Length 82;
Best Local Similarity 41.3%; Pred. No. 0.04;
Matches 19; Conservative 5; Mismatches 8; Indels 14; Gaps 3;

```
Qy          1 DAEFRHDSGYEV---KI-----SITEIKGVIVHR------IETILF 32
              |||||||||||   |:      :   || |:        | |::|
Db         18 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIF 63
```

RESULT 2
Q9UCC8

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ID   Q9UCC8      PRELIMINARY;      PRT;    19 AA.
AC   Q9UCC8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid-(1-42) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94068497; PubMed=8248178;
RA   Roher A.E., Lowenson J.D., Clarke S., Woods A.S., Cotter R.J.,
RA   Gowing E., Ball M.J.;
RT   "beta-Amyloid-(1-42) is a major component of cerebrovascular amyloid
RT   deposits: implications for the pathology of Alzheimer disease.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:10836-10840(1993).
DR   HSSP; P05067; 1AMB.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   19 AA;  2315 MW;  05B02B3F6DDECE3E CRC64;

  Query Match             41.0%;  Score 66;  DB 4;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db          1 DAEFRHDSGYEV 12


RESULT 3
Q9UCD1
ID   Q9UCD1      PRELIMINARY;      PRT;    28 AA.
AC   Q9UCD1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94045685; PubMed=8229004;
RA   Vigo-Pelfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;
RT   "Characterization of beta-amyloid peptide from human cerebrospinal
RT   fluid.";
RL   J. Neurochem. 61:1965-1968(1993).
DR   HSSP; P05067; 1AMB.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   28 AA;  3244 MW;  DE7BD081160AFC81 CRC64;

  Query Match             41.0%;  Score 66;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.017;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db          1 DAEFRHDSGYEV 12


RESULT 4
Q9UCA9
ID   Q9UCA9      PRELIMINARY;      PRT;    30 AA.
AC   Q9UCA9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94153015; PubMed=8109908;
RA   Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;
RT   "The amino acid sequence of neuritic plaque amyloid from a familial
RT   Alzheimer's disease patient.";
RL   Ann. Neurol. 35:245-246(1994).
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   30 AA;  3391 MW;  FF4167ABD081160A CRC64;

  Query Match             41.0%;  Score 66;  DB 4;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.018;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db          1 DAEFRHDSGYEV 12


RESULT 5
Q9UC33
ID   Q9UC33      PRELIMINARY;      PRT;    33 AA.
AC   Q9UC33;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=93024877; PubMed=1406936;
RA   Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA   Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT   "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT   biological fluids.";
RL   Nature 359:325-327(1992).
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   33 AA;  3674 MW;  B1DEFE2F4167ABD0 CRC64;

  Query Match             41.0%;  Score 66;  DB 4;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 0.02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db          1 DAEFRHDSGYEV 12


RESULT 6
Q16020
ID   Q16020      PRELIMINARY;      PRT;    82 AA.
AC   Q16020;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
GN   BETA APP.
OS   Homo sapiens (Human).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S61383; AAB26265.2; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8882 MW;  F534AA5AE5D9230A CRC64;

  Query Match             41.0%;  Score 66;  DB 4;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 0.056;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db         18 DAEFRHDSGYEV 29


RESULT 7
Q16019
ID   Q16019      PRELIMINARY;      PRT;    82 AA.
AC   Q16019;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
GN   BETA APP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S61380; AAB26264.2; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1..
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8938 MW;  F534AA50E579230A CRC64;

  Query Match             41.0%;  Score 66;  DB 4;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 0.056;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db         18 DAEFRHDSGYEV 29


RESULT 8
Q8JH58
ID   Q8JH58      PRELIMINARY;      PRT;   113 AA.
AC   Q8JH58;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid beta protein (Fragment).
OS   Chelydra serpentina serpentina (common snapping turtle).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX   NCBI_TaxID=134619;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21876906; PubMed=11882478;
RA   Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT   "Octylphenol (OP) alters the expression of members of the amyloid
RT   protein family in the hypothalamus of the snapping turtle, Chelydra
RT   serpentina serpentina.";
RL   Environ. Health Perspect. 110:269-275(2002).
DR   EMBL; AF541917; AAN04908.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   113 AA;  12750 MW;  72515C930496E053 CRC64;

  Query Match             41.0%;  Score 66;  DB 13;  Length 113;
  Best Local Similarity   100.0%;  Pred. No. 0.08;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db         15 DAEFRHDSGYEV 26


RESULT 9
O93296
ID   O93296      PRELIMINARY;      PRT;   534 AA.
AC   O93296;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid protein (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98337885; PubMed=9671674;
RA   Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA   Milligan C.E.;
RT   "Increased production of amyloid precursor protein provides a
RT   substrate for caspase-3 in dying motoneurons.";
RL   J. Neurosci. 18:5869-5880(1998).
DR   EMBL; AF042098; AAC25052.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   534 AA;  60597 MW;  FB53ECC2E66D4C92 CRC64;

  Query Match             41.0%;  Score 66;  DB 13;  Length 534;
  Best Local Similarity   100.0%;  Pred. No. 0.46;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
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```
Db        436 DAEFRHDSGYEV 447


RESULT 10
Q9PVL1
ID   Q9PVL1      PRELIMINARY;      PRT;   569 AA.
AC   Q9PVL1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid protein (Fragment).
GN   APP.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT   "What the evolution of the amyloid protein precursor supergene family
RT   tells us about its function.";
RL   Neurochem. Int. 0:0-0(2000).
DR   EMBL; AF030341; AAF12698.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER      1      1
SQ   SEQUENCE   569 AA;  64753 MW;  0AB8BB851863A19D CRC64;

  Query Match             41.0%;  Score 66;  DB 13;  Length 569;
  Best Local Similarity   100.0%;  Pred. No. 0.49;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db        472 DAEFRHDSGYEV 483


RESULT 11
Q9DGJ8
ID   Q9DGJ8      PRELIMINARY;      PRT;   695 AA.
AC   Q9DGJ8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid precursor protein 695 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289218; AAG00593.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   695 AA;  78565 MW;  F201ED02AEC86D95 CRC64;

  Query Match             41.0%;  Score 66;  DB 13;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 0.62;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db        597 DAEFRHDSGYEV 608


RESULT 12
Q9DGJ7
ID   Q9DGJ7      PRELIMINARY;      PRT;   751 AA.
AC   Q9DGJ7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid precursor protein 751 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289219; AAG00594.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   751 AA;  84705 MW;  E78E9413A8033D84 CRC64;

  Query Match             41.0%;  Score 66;  DB 13;  Length 751;
  Best Local Similarity   100.0%;  Pred. No. 0.68;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEV 12
              ||||||||||||
Db        653 DAEFRHDSGYEV 664


RESULT 13
Q66147
ID   Q66147      PRELIMINARY;      PRT;   552 AA.
AC   Q66147;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fusion protein precursor.
OS   Cetacean morbillivirus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=36410;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=porpoise;
RX   MEDLINE=95159670; PubMed=7531923;
RA   Bolt G.G.B., Blixenkrone-Moller M.M.B., Gottschalck E., Wishaupt R.G.,
RA   Welsh M.J., Earle J.A.P., Rima B.K.;
RT   "Nucleotide and deduced amino acid sequences of the matrix (M) and
RT   fusion (F) protein genes of cetacean morbilliviruses isolated from a
RT   porpoise and a dolphin.";
RL   Virus Res. 34:291-304(1994).
DR   EMBL; X80757; CAA56731.1; -.
DR   PIR; S47034; S47034.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Signal.
FT   SIGNAL       1     25       POTENTIAL.
SQ   SEQUENCE   552 AA;  60025 MW;  40D9191AD910EA1E CRC64;

  Query Match             40.1%;  Score 64.5;  DB 12;  Length 552;
  Best Local Similarity   44.8%;  Pred. No. 0.8;
  Matches   13;  Conservative    7;  Mismatches    4;  Indels    5;  Gaps    1;

Qy          9 GYEVKISI-----TEIKGVIVHRIETILF 32
              || : :||     :|:|||||:| : :
Db        278 GYFIVLSIAYPTLSEVKGVIVHRLEAVSY 306
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```
RESULT 14
Q66409
ID   Q66409      PRELIMINARY;      PRT;   552 AA.
AC   Q66409;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Envelope glycoprotein.
GN   F.
OS   Dolphin morbillivirus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=37131;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95159670; PubMed=7531923;
RA   Bolt G.G.B., Blixenkrone-Moller M.M.B., Gottschalck E., Wishaupt R.G.,
RA   Welsh M.J., Earle J.A.P., Rima B.K.;
RT   "Nucleotide and deduced amino acid sequences of the matrix (M) and
RT   fusion (F) protein genes of cetacean morbilliviruses isolated from a
RT   porpoise and a dolphin.";
RL   Virus Res. 34:291-304(1994).
DR   EMBL; Z30086; CAA82903.1; -.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
SQ   SEQUENCE   552 AA;  59869 MW;  40298B33C392ADCD CRC64;

  Query Match             38.2%;  Score 61.5;  DB 12;  Length 552;
  Best Local Similarity   41.4%;  Pred. No. 2.2;
  Matches   12;  Conservative    8;  Mismatches    4;  Indels    5;  Gaps    1;

Qy          9 GYEVKISI-----TEIKGVIVHRIETILF 32
              || : :||     :|:||||||:| : :
Db        278 GYFIVLSIAYPTLSEVKGVIVHKLEAVSY 306
```

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RESULT 15
O56852
ID   O56852      PRELIMINARY;      PRT;   552 AA.
AC   O56852;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   F protein.
OS   Dolphin morbillivirus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=37131;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=D15a from;
RA   Soethout E., Harder T.C., Osterhaus A.D.M.E.;
RT   "Expression of dolphin morbillivirus F and H genes in vaccina virus.";
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ224704; CAA12077.1; -.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
SQ   SEQUENCE   552 AA;  59770 MW;  80FF6A0F25AF3589 CRC64;

  Query Match             38.2%;  Score 61.5;  DB 12;  Length 552;
  Best Local Similarity   41.4%;  Pred. No. 2.2;
  Matches   12;  Conservative    8;  Mismatches    4;  Indels    5;  Gaps    1;

Qy          9 GYEVKISI-----TEIKGVIVHRIETILF 32
              || : :||     :|:||||||:| : :
Db        278 GYFIVLSIAYPTLSEVKGVIVHKLEAVSY 306


Search completed: June 18, 2004, 20:02:29
Job time : 32.0184 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:20 ; Search time 49.0184 Seconds
(without alignments)
195.980 Million cell updates/sec

Title: US-09-865-294A-73
Perfect score: 177
Sequence: 1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	177	100.0	34	6	AAE35679	Aae35679 Human Abe
2	163	92.1	34	6	AAE35681	Aae35681 Human Abe
3	160	90.4	48	6	AAE35680	Aae35680 Human Abe
4	156	88.1	34	6	AAE35682	Aae35682 Human Abe
5	150	84.7	32	6	AAE35678	Aae35678 Human Abe
6	140	79.1	30	6	AAE35677	Aae35677 Human Abe
7	90	50.8	19	6	AAE35657	Aae35657 Measles v
8	90	50.8	31	7	ADD89946	Add89946 CD4 pepti
9	90	50.8	45	7	ADD89951	Add89951 IgE pepti
10	90	50.8	50	7	ADD89944	Add89944 CD4 pepti
11	89.5	50.6	35	2	AAW02335	Aaw02335 Beta-amyl
12	89.5	50.6	35	2	AAW89355	Aaw89355 Beta-amyl
13	89.5	50.6	35	5	ABG71015	Abg71015 Long form
14	89.5	50.6	35	5	ABB05163	Abb05163 Beta amyl
15	89	50.3	63	7	ADB33538	Adb33538 APP regio
16	89	50.3	63	7	ADB33537	Adb33537 APP regio
17	89	50.3	783	7	ADB33505	Adb33505 Human APP
18	89	50.3	783	7	ADB33503	Adb33503 Human APP
19	89	50.3	941	7	ADB33507	Adb33507 Human APP
20	89	50.3	941	7	ADB33509	Adb33509 Human APP
21	88.5	50.0	41	2	AAR45230	Aar45230 Beta amyl
22	88	49.7	26	7	ADE36573	Ade36573 APP epito
23	88	49.7	798	4	ABG19088	Abg19088 Novel hum
24	87.5	49.4	35	2	AAW89360	Aaw89360 Beta-amyl
25	87	49.2	40	5	AAO18462	Aao18462 Human bet
26	87	49.2	42	5	AAO18463	Aao18463 Human bet
27	87	49.2	65	7	ADD89953	Add89953 Foot-and-
28	86	48.6	35	2	AAW89359	Aaw89359 Beta-amyl
29	85.5	48.3	41	2	AAR22206	Aar22206 Alzheimer
30	85	48.0	51	2	AAW53984	Aaw53984 Human ALZ
31	85	48.0	100	5	AAE14375	Aae14375 Amyloid p
32	85	48.0	108	5	AAE14383	Aae14383 Gamma-sec
33	85	48.0	112	2	AAR93556	Aar93556 Familial
34	85	48.0	162	1	AAP83151	Aap83151 Deduced s
35	85	48.0	162	2	AAR10023	Aar10023 Beta-amyl
36	85	48.0	162	2	AAR37863	Aar37863 Deduced f
37	85	48.0	695	2	AAR05166	Aar05166 Sequence
38	85	48.0	695	2	AAW19484	Aaw19484 APP695 mu
39	85	48.0	695	2	AAW19498	Aaw19498 APP695 mu
40	85	48.0	695	3	AAY88436	Aay88436 Human APP
41	85	48.0	695	4	AAU07207	Aau07207 Human bet
42	85	48.0	695	4	AAE10634	Aae10634 Human amy
43	85	48.0	695	4	AAE06864	Aae06864 Human amy
44	85	48.0	695	4	AAE02586	Aae02586 Human amy
45	85	48.0	695	4	AAU06608	Aau06608 Human Amy

ALIGNMENTS

RESULT 1
AAE35679
ID AAE35679 standard; peptide; 34 AA.
XX
AC AAE35679;
XX
DT 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)
XX
DE Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #3.
XX
KW Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS Homo sapiens.
OS Measles virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1. .14
FT /note= "Human beta amyloid peptide"
FT Region 18. .34
FT /note= "Measles virus T helper cell epitope"
XX
PN WO200296350-A2.
XX
PD 05-DEC-2002.
XX
PF 02-APR-2002; 2002WO-US010293.
XX
PR 25-MAY-2001; 2001US-00865294.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2003-201258/19.
XX
PT Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.
XX
PS Claim 9; Page 39; 77pp; English.
XX
CC The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a

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CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 34 AA;

  Query Match             100.0%;  Score 177;  DB 6;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-20;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34
              ||||||||||||||||||||||||||||||||||
Db          1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34


RESULT 2
AAE35681
ID   AAE35681 standard; peptide; 34 AA.
XX
AC   AAE35681;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #5.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .14
FT                   /note= "Human beta amyloid peptide"
FT   Region          18. .34
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Disclosure; Page 39; 77pp; English.
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 34 AA;

  Query Match             92.1%;  Score 163;  DB 6;  Length 34;
  Best Local Similarity   91.2%;  Pred. No. 6.4e-18;
  Matches   31;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34
              |||||||||||||||||:|||||||:|| |||
Db          1 DAEFRHDSGYEVHHKISISEIKGVIVHKIEGILF 34


RESULT 3
AAE35680
ID   AAE35680 standard; peptide; 48 AA.
XX
AC   AAE35680;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #4.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .28
FT                   /note= "Human beta amyloid peptide"
FT   Region          32. .48
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Claim 9; Page 39; 77pp; English.
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```
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 48 AA;

  Query Match             90.4%;  Score 160;  DB 6;  Length 48;
  Best Local Similarity   70.8%;  Pred. No. 2.9e-17;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels   14;  Gaps    1;

Qy          1 DAEFRHDSGYEVHH--------------KISITEIKGVIVHRIETILF 34
              ||||||||||||||              ||||||||||||||||||||
Db          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48


RESULT 4
AAE35682
ID   AAE35682 standard; peptide; 34 AA.
XX
AC   AAE35682;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #6.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .14
FT                   /note= "Human beta amyloid peptide"
FT   Region          18. .34
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Disclosure; Page 39; 77pp; English.
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 34 AA;

  Query Match             88.1%;  Score 156;  DB 6;  Length 34;
  Best Local Similarity   91.2%;  Pred. No. 7.8e-17;
  Matches   31;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34
              ||||||||||||||||||||: ||| |||||||
Db          1 DAEFRHDSGYEVHHKISITEIRTVIVTRIETILF 34


RESULT 5
AAE35678
ID   AAE35678 standard; peptide; 32 AA.
XX
AC   AAE35678;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #2.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .12
FT                   /note= "Human beta amyloid peptide"
FT   Region          16. .32
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
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PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Claim 9; Page 39; 77pp; English.
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 32 AA;

  Query Match             84.7%;  Score 150;  DB 6;  Length 32;
  Best Local Similarity   94.1%;  Pred. No. 6.2e-16;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34
              ||||||||||||  ||||||||||||||||||||
Db          1 DAEFRHDSGYEV--KISITEIKGVIVHRIETILF 32


RESULT 6
AAE35677
ID   AAE35677 standard; peptide; 30 AA.
XX
AC   AAE35677;
XX
DT   23-OCT-2003  (revised)
DT   17-JUN-2003  (first entry)
XX
DE   Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #1.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS   Homo sapiens.
OS   Measles virus.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .10
FT                   /note= "Human beta amyloid peptide"
FT   Region          14. .30
FT                   /note= "Measles virus T helper cell epitope"
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Claim 9; Page 39; 77pp; English.
XX
CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is human Abeta peptide-measles virus T helper cell epitope
CC   fusion peptide immunogen used in the exemplification of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 30 AA;

  Query Match             79.1%;  Score 140;  DB 6;  Length 30;
  Best Local Similarity   88.2%;  Pred. No. 2e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    4;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34
              ||||||||||    ||||||||||||||||||||
Db          1 DAEFRHDSGY----KISITEIKGVIVHRIETILF 30


RESULT 7
AAE35657
ID   AAE35657 standard; peptide; 19 AA.
XX
AC   AAE35657;
XX
DT   17-JUN-2003  (first entry)
XX
DE   Measles virus T helper cell epitope #31.
XX
KW   Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW   Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW   vaccine; nootropic.
XX
OS   Measles virus.
XX
PN   WO200296350-A2.
XX
PD   05-DEC-2002.
XX
PF   02-APR-2002; 2002WO-US010293.
XX
PR   25-MAY-2001; 2001US-00865294.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2003-201258/19.
XX
PT   Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT   fragment of amyloid beta peptide linked to the epitope, and optionally a
PT   spacer, useful for preventing or treating Alzheimer's disease.
XX
PS   Claim 1; Page 37; 77pp; English.
XX
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CC   The present invention relates to a novel peptide immunogen comprising a
CC   helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC   (Abeta) peptide (residues 1-42) linked to the epitope and optionally a
CC   spacer consisting of at least an amino acid to separate the immunogenic
CC   domains. Sequences of the invention are useful for preventing or treating
CC   Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC   peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC   plaques formed from it. They are useful for eliciting a site-directed
CC   mutagenesis against the main functional/regulatory site of the Abeta
CC   peptide and for generating antibodies, which are highly cross-reactive to
CC   the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC   Alzheimer's disease patients. The sequences are useful for induction of
CC   accelerated clearance of amyloid plaques and immunoneutralisation of the
CC   soluble Abeta derived toxins in the brain to prevent and treat
CC   Alzheimer's disease. They are also useful as vaccines. The present
CC   sequence is measles virus T helper (Th) cell epitope used in the
CC   exemplification of the invention
XX
SQ   Sequence 19 AA;

  Query Match             50.8%;  Score 90;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-07;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 ISITEIKGVIVHRIETILF 34
              ||||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 8
ADD89946
ID   ADD89946 standard; protein; 31 AA.
XX
AC   ADD89946;
XX
DT   29-JAN-2004  (first entry)
XX
DE   CD4 peptide used in immunostimulant complex for anti-HIV vaccine.
XX
KW   Immunostimulant; vaccine; human; immunogen; anti-HIV; immunotherapy; CD4.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   20
FT                   /note= "Epsilon-lysine"
XX
PN   WO2003068169-A2.
XX
PD   21-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004711.
XX
PR   14-FEB-2002; 2002US-00076674.
PR   31-JAN-2003; 2003US-00076674.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Sokoll KK;
XX
DR   WPI; 2003-778890/73.
XX
PT   Stabilized immunostimulating complex, useful for vaccination, e.g.
PT   against human immune deficiency viruses, comprises cationic peptide
PT   immunogen and anionic oligonucleotide.
XX
PS   Claim 14; SEQ ID NO 6; 159pp; English.
XX
CC   The present sequence is that of a synthetic immunogenic peptide derived
CC   from human CD4. This is an example of peptides that can be used in
CC   claimed immunostimulatory complexes of the invention that are
CC   specifically adapted to act as adjuvant and as peptide immunogen
CC   stabiliser. The complexes comprise a CpG oligonucleotide and a
CC   biologically active peptide immunogen. The complex is particulate and can
CC   efficiently present peptide immunogens to the cells of the immune system
CC   to produce an immune response. The complexes may be prepared with various
CC   ratios of peptides to CpG oligonucleotides to provide different physical
CC   properties, such as the size of the microparticle. An immunostimulatory
CC   complex comprising the present CD4 derived peptide can be used in an anti
CC   -CD4 immunotherapeutic vaccine for the treatment of HIV infection.
XX
SQ   Sequence 31 AA;

  Query Match             50.8%;  Score 90;  DB 7;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 ISITEIKGVIVHRIETILF 34
              ||||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 9
ADD89951
ID   ADD89951 standard; protein; 45 AA.
XX
AC   ADD89951;
XX
DT   29-JAN-2004  (first entry)
XX
DE   IgE peptide used in immunostimulant complex for allergy vaccine.
XX
KW   Immunostimulant; vaccine; human; immunogen; IgE; immunotherapy; allergy;
KW   antibody; antiallergic.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   20
FT                   /note= "Epsilon-lysine"
XX
PN   WO2003068169-A2.
XX
PD   21-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004711.
XX
PR   14-FEB-2002; 2002US-00076674.
PR   31-JAN-2003; 2003US-00076674.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Sokoll KK;
XX
DR   WPI; 2003-778890/73.
XX
PT   Stabilized immunostimulating complex, useful for vaccination, e.g.
PT   against human immune deficiency viruses, comprises cationic peptide
PT   immunogen and anionic oligonucleotide.
XX
PS   Claim 20; SEQ ID NO 11; 159pp; English.
XX
CC   The present sequence is that of a synthetic immunogenic peptide derived
CC   from human IgE. This is an example of peptides that can be used in
CC   claimed immunostimulatory complexes of the invention that are
CC   specifically adapted to act as adjuvant and as peptide immunogen
CC   stabiliser. The complexes comprise a CpG oligonucleotide and a
CC   biologically active peptide immunogen. The complex is particulate and can
CC   efficiently present peptide immunogens to the cells of the immune system
CC   to produce an immune response. The complexes may be prepared with various
CC   ratios of peptides to CpG oligonucleotides to provide different physical
CC   properties, such as the size of the microparticle. An immunostimulatory
CC   complex comprising the present IgE derived peptide can be used in an anti
CC   -IgE immunotherapeutic vaccine for the treatment of allergy.
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XX
SQ   Sequence 45 AA;

  Query Match             50.8%;  Score 90;  DB 7;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 ISITEIKGVIVHRIETILF 34
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 10
ADD89944
ID   ADD89944 standard; protein; 50 AA.
XX
AC   ADD89944;
XX
DT   29-JAN-2004  (first entry)
XX
DE   CD4  peptide used in immunostimulant complex as anti-HIV vaccine.
XX
KW   Immunostimulant; vaccine; human; immunogen; anti-HIV; immunotherapy.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   20
FT                   /note= "Epsilon-lysine"
XX
PN   WO2003068169-A2.
XX
PD   21-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004711.
XX
PR   14-FEB-2002; 2002US-00076674.
PR   31-JAN-2003; 2003US-00076674.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Sokoll KK;
XX
DR   WPI; 2003-778890/73.
XX
PT   Stabilized immunostimulating complex, useful for vaccination, e.g.
PT   against human immune deficiency viruses, comprises cationic peptide
PT   immunogen and anionic oligonucleotide.
XX
PS   Claim 14; SEQ ID NO 4; 159pp; English.
XX
CC   The present sequence is that of a synthetic immunogenic peptide derived
CC   from human CD4. This is an example of peptides that can be used in
CC   claimed immunostimulatory complexes of the invention that are
CC   specifically adapted to act as adjuvant and as peptide immunogen
CC   stabiliser. The complexes comprise a CpG oligonucleotide and a
CC   biologically active peptide immunogen. The complex is particulate and can
CC   efficiently present peptide immunogens to the cells of the immune system
CC   to produce an immune response. The complexes may be prepared with various
CC   ratios of peptides to CpG oligonucleotides to provide different physical
CC   properties, such as the size of the microparticle. An immunostimulatory
CC   complex comprising the present CD4 derived peptide can be used in an anti
CC   -CD4 immunotherapeutic vaccine for the treatment of HIV infection.
XX
SQ   Sequence 50 AA;

  Query Match             50.8%;  Score 90;  DB 7;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 ISITEIKGVIVHRIETILF 34
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 11
AAW02335
ID   AAW02335 standard; peptide; 35 AA.
XX
AC   AAW02335;
XX
DT   06-MAY-1997  (first entry)
XX
DE   Beta-amyloid peptide residues 1-20, 26-40.
XX
KW   Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
KW   cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
KW   familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
KW   isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
KW   bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
KW   adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
KW   scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
XX
OS   Synthetic.
XX
PN   WO9628471-A1.
XX
PD   19-SEP-1996.
XX
PF   14-MAR-1996;   96WO-US003492.
XX
PR   14-MAR-1995;   95US-00404831.
PR   07-JUN-1995;   95US-00475579.
PR   27-OCT-1995;   95US-00548998.
XX
PA   (PHAR-) PHARM PEPTIDES INC.
XX
PI   Findeis MA,  Benjamin H,  Garnick MB,  Gefter ML,  Hundal A;
PI   Kasman L,  Musso G,  Signer ER,  Wakefield J,  Reed MJ,  Molineaux S;
PI   Kubasek W,  Chin J,  Lee J,  Kelley M;
XX
DR   WPI; 1996-433762/43.
XX
PT   Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
PT   protein coupled (in)directly to at least 1 modifying gp., useful in
PT   treatment of Alzheimer's disease.
XX
PS   Claim 29; Page 82; 106pp; English.
XX
CC   AAW02333-W02336 represent beta-amyloid peptide fragments that can be used
CC   in the modulator compounds of the invention. Beta-amyloid peptide is a 4
CC   kilodalton peptide that is the major protein component of amyloid
CC   plaques. Amyloid plaques are present both in the brain lesions, and in
CC   the walls of cerebral blood vessels in Alzheimer's disease patients. The
CC   amyloid modulators of the invention comprise an amyloidogenic protein or
CC   peptide (see AAW02310-W02336) coupled directly or indirectly to at least
CC   one modifying group. The modifying group is preferably a cyclic,
CC   heterocyclic, or polycyclic group, such as declain, a cholanyl group, a
CC   biotin containing group, or a fluorescein containing group. These
CC   compounds then modulate the aggregation of these sequences to natural
CC   amyloid proteins or peptides when contacted with the natural
CC   amyloidogenic proteins or peptides. The modulator compounds can be used
CC   in the treatment of disorders associated with amyloidosis, such as
CC   familial amyloid polyneuropathy, familial amyloid cardiomyopathy,
CC   isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
CC   bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
CC   diabetes, insulinoma, familial Mediterranean fever, familial amyloid
CC   nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
CC   and other types of amyloidosis. The modulators are also useful for the
CC   treatment of disorders associated with beta-amyloidosis, especially
CC   Alzheimer's disease
XX
SQ   Sequence 35 AA;

  Query Match             50.6%;  Score 89.5;  DB 2;  Length 35;
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  Best Local Similarity   66.7%;  Pred. No. 1.8e-06;
  Matches   18;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 DAEFRHDSGYEVHH-KISITEIKGVIV 26
              ||||||||||||| |:     || |:
Db          1 DAEFRHDSGYEVHHQKLVFFSNKGAII 27


RESULT 12
AAW89355
ID   AAW89355 standard; peptide; 35 AA.
XX
AC   AAW89355;
XX
DT   02-MAR-1999  (first entry)
XX
DE   Beta-amyloid peptide derivative A-beta-1-20,26-40.
XX
KW   Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
KW   aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
KW   familial amyloid polyneuropathy; bovine spongiform encephalopathy;
KW   Creutzfeldt-Jakob disease; bAP.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US5854204-A.
XX
PD   29-DEC-1998.
XX
PF   14-MAR-1996;   96US-00612785.
XX
PR   14-MAR-1995;   95US-00404831.
PR   07-JUN-1995;   95US-00475579.
PR   27-OCT-1995;   95US-00548998.
XX
PA   (PRAE-) PRAECIS PHARM INC.
XX
PI   Hundal A,  Gefter ML,  Kasman L,  Musso G,  Molineaux S,  Benjamin H;
PI   Findeis MA,  Chin J,  Lee J,  Kelley M,  Reed M,  Wakefield J;
PI   Garnick MB,  Kubasek W,  Signer ER;
XX
DR   WPI; 1999-094964/08.
XX
PT   New peptide(s) derived from beta-amyloid peptide that inhibit amyloid
PT   aggregation - and neurotoxicity, specifically for treatment and
PT   prevention of Alzheimer's disease.
XX
PS   Claim 3; Col 71-72; 52pp; English.
XX
CC   The present invention describes beta-amyloid peptide (bAP) derivatives.
CC   The bAP derivatives inhibit aggregation of amyloidogenic proteins and
CC   peptides, specifically bAP, and their neurotoxicity, so are useful for
CC   treating and preventing any disease involving amyloidosis, specifically
CC   Alzheimer's disease but also Down's syndrome, familial amyloid
CC   polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and
CC   Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
CC   these diseases, in vitro or in vivo, by detecting binding of bAP to
CC   labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
CC   even when bAP is present in molar excess. The present sequence represents
CC   a bAP derivative
XX
SQ   Sequence 35 AA;

  Query Match             50.6%;  Score 89.5;  DB 2;  Length 35;
  Best Local Similarity   66.7%;  Pred. No. 1.8e-06;
  Matches   18;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 DAEFRHDSGYEVHH-KISITEIKGVIV 26
              ||||||||||||| |:     || |:
Db          1 DAEFRHDSGYEVHHQKLVFFSNKGAII 27


RESULT 13
ABG71015
ID   ABG71015 standard; peptide; 35 AA.
XX
AC   ABG71015;
XX
DT   05-DEC-2002  (first entry)
XX
DE   Long form beta-amyloid protein fragment, mutant #2.
XX
KW   Beta-amyloid; amyloid modulator; amyloidogenic protein; amyloidosis;
KW   familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
KW   isolated cardiac amyloid; systemic senile amyloidosis; scrapie; myeloma;
KW   bovine spongiform encephalopathy; BSE; Creutzfeldt-Jakob disease;
KW   adult onset diabetes; Gerstmann-Straussler-Scheinker syndrome;
KW   insulinoma; atrial amyloidosis; idiopathic amyloidosis; haemodialysis;
KW   macroglobulinaemia-associated amyloidosis; reactive amyloidosis;
KW   primary localised cutaneous nodular amyloidosis; Sjogren's syndrome;
KW   hereditary cerebral haemorrhage with amyloidosis; Muckle-Wells syndrome;
KW   hereditary non-neuropathic systemic amyloidosis;
KW   familial Mediterranean Fever; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1. .20
FT                   /note= "Residues 1-20 of Beta-amyloid (ABG71001)"
FT   Misc-difference 21. .35
FT                   /note= "Residues 26-40 of beta-amyloid (ABG71001)"
XX
PN   US2002098173-A1.
XX
PD   25-JUL-2002.
XX
PF   04-OCT-2001; 2001US-00972475.
XX
PR   14-MAR-1995;   95US-00404831.
PR   07-JUN-1995;   95US-00475579.
PR   27-OCT-1995;   95US-00548998.
PR   14-MAR-1996;   96US-00617267.
XX
PA   (PRAE-) PRAECIS PHARM INC.
XX
PI   Findeis MA,  Benjamin H,  Garnick MB,  Gefter ML,  Hundal A;
PI   Kasman L,  Musso G,  Signer ER,  Wakefield J,  Reed MJ;
XX
DR   WPI; 2002-697709/75.
XX
PT   Amyloid modulator useful for treating a disorder associated with
PT   amyloidosis, comprises an amyloidogenic protein and/or a peptide fragment
PT   coupled to a modifying group.
XX
PS   Example 12; Page; 41pp; English.
XX
CC   The invention describes an amyloid modulator comprising an amyloidogenic
CC   protein and/or peptide fragment coupled to a modifying group so that the
CC   compound modulates the aggregation of natural amyloid proteins or
CC   peptides. The modulator is used for treating a disorder associated with
CC   amyloidosis e.g. familial amyloid polyneuropathy (Portuguese, Japanese
CC   and Swedish types), familial amyloid cardiomyopathy (Danish type),
CC   isolated cardiac amyloid, systemic senile amyloidosis, scrapie, bovine
CC   spongiform encephalopathy, Creutzfeldt-Jakob disease, adult onset
CC   diabetes, Gerstmann-Straussler-Scheinker syndrome, insulinoma, isolated
CC   atrial amyloidosis, idiopathic (primary) amyloidosis, myeloma or
CC   macroglobulinaemia-associated amyloidosis, primary localised cutaneous
CC   nodular amyloidosis associated with Sjogren's syndrome, reactive
CC   (secondary) amyloidosis, familial Mediterranean Fever and familial
CC   amyloid nephropathy with urticaria and deafness (Muckle-Wells syndrome),
CC   hereditary cerebral haemorrhage with amyloidosis of Icelandic type,
CC   amyloidosis associated with long term haemodialysis, hereditary non-
CC   neuropathic systemic amyloidosis (familial amyloid polyneuropathy III),
CC   familial amyloidosis of Finnish type, amyloidosis associated with
```

CC medullary carcinoma of the thyroid, fibrinogen-associated hereditary
CC renal amyloidosis and lysozyme-associated hereditary systemic
CC amyloidosis. The compound is capable of altering and inhibiting beta-
CC amyloid protein (beta-AP) aggregation of natural amyloidogenic proteins
CC or peptides when contacted with a molar excess amount of natural beta-APs
CC relative to the modulator. This sequence represents a mutant of the long
CC form of beta-amyloid used in the creation of an amyloid modulator. Note:
CC This sequence does not appear in the specification but has been created
CC from the wild type sequence (ABG71001) using information given in the
CC invention
XX
SQ Sequence 35 AA;

Query Match 50.6%; Score 89.5; DB 5; Length 35;
Best Local Similarity 66.7%; Pred. No. 1.8e-06;
Matches 18; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy 1 DAEFRHDSGYEVHH-KISITEIKGVIV 26
||||||||||||||| |: || |:
Db 1 DAEFRHDSGYEVHHQKLVFFSNKGAII 27

RESULT 14
ABB05163
ID ABB05163 standard; peptide; 35 AA.
XX
AC ABB05163;
XX
DT 02-APR-2002 (first entry)
XX
DE Beta amyloid peptide (1-20,26-40) SEQ ID NO:15.
XX
KW Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta;
KW APP-770; amyloid aggregation; amyloidogenic; Alzheimer's disease;
KW nootropic; neuroprotective; immunosuppressive; antimicrobial; auditory;
KW antidiabetic; antipyretic; dermatological; cardiovascular; nephrotropic;
KW amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome;
KW amyloidogenic disease; beta amyloid deposition; amyloidosis;
KW hereditary cerebral haemorrhage; familial amyloid polyneuropathy.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6319498-B1.
XX
PD 20-NOV-2001.
XX
PF 14-MAR-1996; 96US-00617267.
XX
PR 14-MAR-1995; 95US-00404831.
PR 07-JUN-1995; 95US-00475579.
PR 27-OCT-1995; 95US-00548998.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PI Findeis MA, Benjamin H, Garnick MB, Gefter ML, Hundal A;
PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;
XX
DR WPI; 2002-146668/19.
XX
PT Amyloid modulator compound useful for treatment of an amyloidogenic
PT disease such as Alzheimer's disease comprises an aggregation core domain
PT and a modifying group attached to it.
XX
PS Disclosure; Col 75; 54pp; English.
XX
CC The present invention describes an amyloid modulator compound (I)
CC comprising an aggregation core domain and a modifying group attached to
CC it. (I) has nootropic, neuroprotective, immunosuppressive, antimicrobial,
CC antidiabetic, antipyretic, dermatological, cardiovascular, nephrotropic
CC and auditory activities, and can be used as a natural amyloid aggregation
CC inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide
CC (beta-AP). (I) are used in the manufacture of a medicament for the
CC diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's
CC disease and other clinical occurrences of beta amyloid deposition such as
CC Down's syndrome individuals and in patients with hereditary cerebral
CC haemorrhage with amyloidosis, and for treating a disorder associated with
CC amyloidosis such as familial amyloid polyneuropathy. (I) reduces the
CC toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)
CC not only reduces the formation of neurotoxic aggregates but also have the
CC ability to reduce the neurotoxicity of performed A-beta fibrils. The
CC present sequence represents a beta-AP peptide, which is used in the
CC exemplification of the present invention
XX
SQ Sequence 35 AA;

Query Match 50.6%; Score 89.5; DB 5; Length 35;
Best Local Similarity 66.7%; Pred. No. 1.8e-06;
Matches 18; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy 1 DAEFRHDSGYEVHH-KISITEIKGVIV 26
||||||||||||||| |: || |:
Db 1 DAEFRHDSGYEVHHQKLVFFSNKGAII 27

RESULT 15
ADB33538
ID ADB33538 standard; protein; 63 AA.
XX
AC ADB33538;
XX
DT 04-DEC-2003 (first entry)
XX
DE APP region SEQ ID NO:37.
XX
KW fusion protein; amyloid precursor protein; APP; transcription factor;
KW nootropic; neuroprotective; APP inhibitor;
KW amyloid precursor protein inhibitor; Alzheimer's disease; beta-secretase;
KW gamma-secretase; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003072041-A2.
XX
PD 04-SEP-2003.
XX
PF 23-FEB-2003; 2003WO-US005458.
XX
PR 27-FEB-2002; 2002US-0360274P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Espeseth AS, Ferrer M, Flores OA, Hazuda DJ, Inglese J;
PI Miller MD, Register B, Shi X, Simon AJ, Zuck PD;
XX
DR WPI; 2003-689968/65.
XX
PT DNA encoding a fusion protein of amyloid precursor protein, useful in
PT screening for anti-Alzheimer agents, comprises a fused transcription
PT factor.
XX
PS Disclosure; Page 18; 193pp; English.
XX
CC The present invention describes a DNA molecule (I) that encodes a fusion
CC protein (FP) comprising: (i) an amino acid sequence of amyloid precursor
CC protein (APP), either the wild type, Swedish or NFEV versions; and (ii) a
CC transcription factor (TF), fused in frame to the C-terminus of (i). Also
CC described: (1) an expression vector containing (I); (2) a eukaryotic cell
CC containing (I); and (3) methods for identifying a compound (A) that
CC inhibits processing of APP, using the cells of (2). (I) has nootropic and
CC neuroprotective activities. (I) can be used to produce eukaryotic cells
CC that express FP and are useful in screening for agents that inhibit
CC processing of APP. The agents are potentially useful for the treatment or
CC prevention of Alzheimer's disease. Cells that express FP can screen for
CC inhibitors of: (a) beta- and gamma-secretases; and (b)

CC cytoplasmic/extracellular APP signaling in a single assay. Cell-based
CC assays may be free of interference from alpha-secretase activity and are
CC homogeneous (no chromatography, immunoprecipitation or washing required)
CC so well suited to high-throughput screening. The present sequence
CC represents a human APP amino acid sequence, which is given in the
CC exemplification of the present invention.
XX
SQ Sequence 63 AA;

Query Match 50.3%; Score 89; DB 7; Length 63;
Best Local Similarity 53.1%; Pred. No. 4.5e-06;
Matches 17; Conservative 4; Mismatches 5; Indels 6; Gaps 1;

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              ||||||||||||||::      :   || |:
Db          9 DAEFRHDSGYEVHHQVLVPFAEDVGSNKGAII 40
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Search completed: June 18, 2004, 19:58:52
Job time : 50.0184 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:54:46 ; Search time 13.3497 Seconds
(without alignments)
131.485 Million cell updates/sec

Title: US-09-865-294A-73
Perfect score: 177
Sequence: 1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	89.5	50.6	35	2	US-08-612-785B-15	Sequence 15, Appl
2	89.5	50.6	35	4	US-08-617-267C-15	Sequence 15, Appl
3	87.5	49.4	35	2	US-08-612-785B-39	Sequence 39, Appl
4	86	48.6	35	2	US-08-612-785B-38	Sequence 38, Appl
5	85.5	48.3	41	1	US-07-819-361-1	Sequence 1, Appli
6	85	48.0	38	6	5262332-1	Patent No. 5262332
7	85	48.0	152	6	5187153-4	Patent No. 5187153
8	85	48.0	162	6	5220013-4	Patent No. 5220013
9	85	48.0	162	6	5223482-4	Patent No. 5223482
10	85	48.0	695	4	US-09-548-372D-14	Sequence 14, Appl
11	85	48.0	695	4	US-09-548-367D-14	Sequence 14, Appl
12	85	48.0	695	4	US-09-551-853D-14	Sequence 14, Appl
13	85	48.0	697	4	US-09-548-372D-20	Sequence 20, Appl
14	85	48.0	697	4	US-09-548-367D-20	Sequence 20, Appl
15	85	48.0	697	4	US-09-551-853D-20	Sequence 20, Appl
16	84.5	47.7	42	1	US-08-268-348A-6	Sequence 6, Appli
17	84	47.5	43	2	US-08-404-831-3	Sequence 3, Appli
18	84	47.5	43	2	US-08-612-785B-3	Sequence 3, Appli
19	84	47.5	43	2	US-08-475-579A-3	Sequence 3, Appli
20	84	47.5	43	4	US-08-617-267C-3	Sequence 3, Appli
21	83	46.9	15	2	US-08-609-090-1	Sequence 1, Appli
22	83	46.9	16	1	US-08-302-808-10	Sequence 10, Appl
23	83	46.9	16	2	US-08-986-948-10	Sequence 10, Appl
24	83	46.9	17	4	US-09-594-366-2	Sequence 2, Appli
25	83	46.9	21	2	US-08-659-984A-18	Sequence 18, Appl
26	83	46.9	21	3	US-08-660-531-18	Sequence 18, Appl
27	83	46.9	27	1	US-08-141-324-11	Sequence 11, Appl
28	83	46.9	27	1	US-08-141-324-12	Sequence 12, Appl
29	83	46.9	27	1	US-08-541-902-11	Sequence 11, Appl
30	83	46.9	27	1	US-08-541-902-12	Sequence 12, Appl
31	83	46.9	28	1	US-08-346-849-4	Sequence 4, Appli
32	83	46.9	28	1	US-08-302-808-7	Sequence 7, Appli
33	83	46.9	28	2	US-08-609-090-2	Sequence 2, Appli
34	83	46.9	28	2	US-08-986-948-7	Sequence 7, Appli
35	83	46.9	28	2	US-08-293-284A-4	Sequence 4, Appli
36	83	46.9	28	2	US-08-461-216-2	Sequence 2, Appli
37	83	46.9	28	3	US-09-388-890-2	Sequence 2, Appli
38	83	46.9	28	3	US-09-388-890-11	Sequence 11, Appl
39	83	46.9	28	3	US-09-388-890-12	Sequence 12, Appl
40	83	46.9	28	3	US-09-388-890-13	Sequence 13, Appl
41	83	46.9	28	3	US-09-388-890-14	Sequence 14, Appl
42	83	46.9	28	4	US-08-723-661B-2	Sequence 2, Appli
43	83	46.9	28	4	US-09-660-954-2	Sequence 2, Appli
44	83	46.9	28	4	US-09-660-954-11	Sequence 11, Appl
45	83	46.9	28	4	US-09-660-954-12	Sequence 12, Appl

ALIGNMENTS

```
RESULT 1
US-08-612-785B-15
; Sequence 15, Application US/08612785B
; Patent No. 5854204
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;    TITLE OF INVENTION:  Aggregation
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,785B
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-08-612-785B-15
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  Query Match             50.6%;  Score 89.5;  DB 2;  Length 35;
  Best Local Similarity   66.7%;  Pred. No. 2.5e-07;
  Matches   18;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 DAEFRHDSGYEVHH-KISITEIKGVIV 26
              ||||||||||||| |:     || |:
Db          1 DAEFRHDSGYEVHHQKLVFFSNKGAII 27


RESULT 2
US-08-617-267C-15
; Sequence 15, Application US/08617267C
; Patent No. 6319498
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of Amyloid Aggregation
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/617,267C
;      FILING DATE:  14-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-08-617-267C-15

  Query Match             50.6%;  Score 89.5;  DB 4;  Length 35;
  Best Local Similarity   66.7%;  Pred. No. 2.5e-07;
  Matches   18;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 DAEFRHDSGYEVHH-KISITEIKGVIV 26
              ||||||||||||| |:     || |:
Db          1 DAEFRHDSGYEVHHQKLVFFSNKGAII 27


RESULT 3
US-08-612-785B-39
; Sequence 39, Application US/08612785B
; Patent No. 5854204
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;    TITLE OF INVENTION:  Aggregation
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,785B
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-08-612-785B-39

  Query Match             49.4%;  Score 87.5;  DB 2;  Length 35;
  Best Local Similarity   63.0%;  Pred. No. 5.1e-07;
  Matches   17;  Conservative    3;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHKI-SITEIKGVIV 26
              |||||||||||||:   :   || |:
Db          1 DAEFRHDSGYEVHHQAEDVGSNKGAII 27


RESULT 4
US-08-612-785B-38
; Sequence 38, Application US/08612785B
; Patent No. 5854204
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;    TITLE OF INVENTION:  Aggregation
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/612,785B
;       FILING DATE:  Herewith
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/404,831
;       FILING DATE:  14-MAR-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/475,579
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/548,998
;       FILING DATE:  27-OCT-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DeConti, Giulio A.
;       REGISTRATION NUMBER:  31,503
;       REFERENCE/DOCKET NUMBER:  PPI-002CP3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)227-7400
;       TELEFAX:  (617)742-4214
;   INFORMATION FOR SEQ ID NO:  38:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  35 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FRAGMENT TYPE:  internal
US-08-612-785B-38

  Query Match             48.6%;  Score 86;  DB 2;  Length 35;
  Best Local Similarity   63.0%;  Pred. No. 8.9e-07;
  Matches   17;  Conservative    3;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHK--ISITEIKGVI 25
              |||||||||||||:  :   |  |:|
Db          1 DAEFRHDSGYEVHHQKLVFFAEDVGII 27


RESULT 5
US-07-819-361-1
; Sequence 1, Application US/07819361
; Patent No. 5338663
;  GENERAL INFORMATION:
;     APPLICANT:  Potter, Huntington
;     APPLICANT:  Kayyali, Usamah
;     TITLE OF INVENTION:  Method of Interfering With Formation of
;     TITLE OF INVENTION:  Alpha-Antichymotrypsin-Beta-Protein Complex, Method of
;     TITLE OF INVENTION:  Inhibiting Beta-Protein Function and Compounds For Use
;     TITLE OF INVENTION:  Therein
;     NUMBER OF SEQUENCES:  6
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;       STREET:  Two Militia Drive
;       CITY:  Lexington
;       STATE:  Massachusetts
;       COUNTRY:  U.S.A.
;       ZIP:  02173
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/819,361
;       FILING DATE:  19920113
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Granahan, Patricia
;       REGISTRATION NUMBER:  32,227
;       REFERENCE/DOCKET NUMBER:  HU90-03A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-861-6240
;       TELEFAX:  617-861-9540
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  41 amino acids
;       TYPE:  AMINO ACID
;       TOPOLOGY:  linear
US-07-819-361-1

  Query Match             48.3%;  Score 85.5;  DB 1;  Length 41;
  Best Local Similarity   54.8%;  Pred. No. 1.3e-06;
  Matches   17;  Conservative    3;  Mismatches    6;  Indels    5;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHK-----ISITEIKGVIV 26
              |||||||||||||:      :   || |:
Db          1 DAEFRHDSGYEVHHQKLVFFADVGSNKGAII 31


RESULT 6
5262332-1
;Patent No. 5262332
;     APPLICANT: SELKOE, DENNIS J.
;     TITLE OF INVENTION: DIAGNOSTIC METHOD FOR ALZHEIMER'S
;DISEASE:EXAMINATION OF NON-NEURAL TISSUE
;     NUMBER OF SEQUENCES: 1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/410,138
;       FILING DATE: 19-SEP-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 333,609
;       FILING DATE: 05-APR-1989
;SEQ ID NO:1:
;       LENGTH: 38
5262332-1

  Query Match             48.0%;  Score 85;  DB 6;  Length 38;
  Best Local Similarity   69.6%;  Pred. No. 1.4e-06;
  Matches   16;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHKISITEIKG 23
              |||||||||||||:   |  |
Db          1 DAEFRHDSGYEVHQKLVFAEDVG 23


RESULT 7
5187153-4
;Patent No. 5187153
;     APPLICANT: CORDELL, BARBARA;SCHILLING, JAMES W.;KATUNUMA, NOBUHIKO
;     TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
;AMYLOID POLYPEPTIDE DERIVATIVES
;     NUMBER OF SEQUENCES: 33
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/502,273
;       FILING DATE: 29-MAR-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 361,912
;       FILING DATE: 06-JUN-1989
;       APPLICATION NUMBER: 359,911
;       FILING DATE: 12-MAY-1989
;       APPLICATION NUMBER: 87,002
;       FILING DATE: 18-AUG-1987
;       APPLICATION NUMBER: 8,810
;       FILING DATE: 30-JAN-1987
;       APPLICATION NUMBER: 948,376
;       FILING DATE: 31-DEC-1986
;       APPLICATION NUMBER: 932,193
;       FILING DATE: 17-NOV-1986
;SEQ ID NO:4:
;       LENGTH: 152
5187153-4

  Query Match             48.0%;  Score 85;  DB 6;  Length 152;
  Best Local Similarity   71.4%;  Pred. No. 8.2e-06;
  Matches   15;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy          1 DAEFRHDSGYEVHHKISITEI 21
              |||||||||||||||:  : :|
Db         74 DAEFRHDSGYEVHHQKLVRKI 94


RESULT 8
5220013-4
;Patent No. 5220013
;     APPLICANT: PONTE, PHYLLIS A.;CORDELL, BARBARA
;     TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
;OF ALZHEIMER'S DISEASE
;     NUMBER OF SEQUENCES: 30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/444,118
;       FILING DATE: 30-NOV-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 87,002
;       FILING DATE: 18-AUG-1987
;       APPLICATION NUMBER: 8,810
;       FILING DATE: 30-JAN-1987
;       APPLICATION NUMBER: 948,376
;       FILING DATE: 31-DEC-1986
;       APPLICATION NUMBER: 932,193
;       FILING DATE: 17-NOV-1986
;SEQ ID NO:4:
;       LENGTH: 162
5220013-4

  Query Match             48.0%;  Score 85;  DB 6;  Length 162;
  Best Local Similarity   71.4%;  Pred. No. 8.9e-06;
  Matches   15;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHKISITEI 21
              |||||||||||||||:  : :|
Db         81 DAEFRHDSGYEVHHQKLVRKI 101


RESULT 9
5223482-4
;Patent No. 5223482
;     APPLICANT: SCHILLING, JAMES W.;PONTE, PHYLLIS A.;CORDELL,
;BARBARA
;     TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
;INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
;     NUMBER OF SEQUENCES: 34
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/361,912
;       FILING DATE: 06-JUN-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 359,911
;       FILING DATE: 12-MAY-1989
;       APPLICATION NUMBER: 87,002
;       FILING DATE: 18-AUG-1987
;       APPLICATION NUMBER: 8,810
;       FILING DATE: 30-JAN-1987
;       APPLICATION NUMBER: 948,376
;       FILING DATE: 31-DEC-1986
;       APPLICATION NUMBER: 932,193
;       FILING DATE: 17-NOV-1986
;SEQ ID NO:4:
;       LENGTH: 162
5223482-4

  Query Match             48.0%;  Score 85;  DB 6;  Length 162;
  Best Local Similarity   71.4%;  Pred. No. 8.9e-06;
  Matches   15;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHKISITEI 21
              |||||||||||||||:  : :|
Db         81 DAEFRHDSGYEVHHQKLVRKI 101


RESULT 10
US-09-548-372D-14
; Sequence 14, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-372D-14

  Query Match             48.0%;  Score 85;  DB 4;  Length 695;
  Best Local Similarity   43.5%;  Pred. No. 5.6e-05;
  Matches   20;  Conservative    5;  Mismatches    9;  Indels   12;  Gaps    2;

Qy          1 DAEFRHDSGYEVHHK------ISITEIKGVIVHR------IETILF 34
              |||||||||||||||:        :   || |:        | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIF 642


RESULT 11
US-09-548-367D-14
; Sequence 14, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-367D-14

  Query Match             48.0%;  Score 85;  DB 4;  Length 695;
  Best Local Similarity   43.5%;  Pred. No. 5.6e-05;
  Matches   20;  Conservative    5;  Mismatches    9;  Indels   12;  Gaps    2;

Qy          1 DAEFRHDSGYEVHHK------ISITEIKGVIVHR------IETILF 34
              |||||||||||||||:        :   || |:        | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIF 642


RESULT 12
US-09-551-853D-14
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; Sequence 14, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280L
;  CURRENT APPLICATION NUMBER: US/09/551,853D
;  CURRENT FILING DATE:  2000-04-18
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-551-853D-14

  Query Match             48.0%;  Score 85;  DB 4;  Length 695;
  Best Local Similarity   43.5%;  Pred. No. 5.6e-05;
  Matches   20;  Conservative    5;  Mismatches    9;  Indels   12;  Gaps    2;

Qy          1 DAEFRHDSGYEVHHK------ISITEIKGVIVHR------IETILF 34
              |||||||||||||||:        :   || |:        | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIF 642


RESULT 13
US-09-548-372D-20
; Sequence 20, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280I
;  CURRENT APPLICATION NUMBER: US/09/548,372D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-372D-20

  Query Match             48.0%;  Score 85;  DB 4;  Length 697;
  Best Local Similarity   43.5%;  Pred. No. 5.6e-05;
  Matches   20;  Conservative    5;  Mismatches    9;  Indels   12;  Gaps    2;

Qy          1 DAEFRHDSGYEVHHK------ISITEIKGVIVHR------IETILF 34
              |||||||||||||||:        :   || |:        | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIF 642


RESULT 14
US-09-548-367D-20
; Sequence 20, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280H
;  CURRENT APPLICATION NUMBER: US/09/548,367D
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-367D-20

  Query Match             48.0%;  Score 85;  DB 4;  Length 697;
  Best Local Similarity   43.5%;  Pred. No. 5.6e-05;
  Matches   20;  Conservative    5;  Mismatches    9;  Indels   12;  Gaps    2;

Qy          1 DAEFRHDSGYEVHHK------ISITEIKGVIVHR------IETILF 34
              |||||||||||||||:        :   || |:        | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIF 642


RESULT 15
US-09-551-853D-20
; Sequence 20, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
;  APPLICANT: GURNEY ET AL.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 29915/6280L
;  CURRENT APPLICATION NUMBER: US/09/551,853D
;  CURRENT FILING DATE:  2000-04-18
;  PRIOR APPLICATION NUMBER: US 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-551-853D-20

  Query Match             48.0%;  Score 85;  DB 4;  Length 697;
  Best Local Similarity   43.5%;  Pred. No. 5.6e-05;
  Matches   20;  Conservative    5;  Mismatches    9;  Indels   12;  Gaps    2;

Qy          1 DAEFRHDSGYEVHHK------ISITEIKGVIVHR------IETILF 34
              |||||||||||||||:        :   || |:        | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIF 642


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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 20:02:36 ; Search time 38.3804 Seconds
(without alignments)
250.093 Million cell updates/sec

Title: US-09-865-294A-73
Perfect score: 177
Sequence: 1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34

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Gapop 10.0 , Gapext 0.5

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	177	100.0	34	10	US-09-865-294-73	Sequence 73, Appl
2	163	92.1	34	10	US-09-865-294-75	Sequence 75, Appl
3	160	90.4	48	10	US-09-865-294-74	Sequence 74, Appl
4	156	88.1	34	10	US-09-865-294-76	Sequence 76, Appl
5	150	84.7	32	10	US-09-865-294-72	Sequence 72, Appl
6	140	79.1	30	10	US-09-865-294-71	Sequence 71, Appl
7	90	50.8	19	10	US-09-865-294-51	Sequence 51, Appl
8	90	50.8	31	14	US-10-076-674-6	Sequence 6, Appli
9	90	50.8	31	15	US-10-355-161A-6	Sequence 6, Appli
10	90	50.8	45	14	US-10-076-674-11	Sequence 11, Appl
11	90	50.8	45	15	US-10-355-161A-11	Sequence 11, Appl
12	90	50.8	50	14	US-10-076-674-4	Sequence 4, Appli
13	90	50.8	50	15	US-10-355-161A-4	Sequence 4, Appli
14	89.5	50.6	35	9	US-09-972-475-15	Sequence 15, Appl
15	89.5	50.6	35	15	US-10-463-729-15	Sequence 15, Appl
16	87	49.2	65	15	US-10-355-161A-13	Sequence 13, Appl
17	85	48.0	100	15	US-10-275-025-5	Sequence 5, Appli
18	85	48.0	108	15	US-10-275-025-13	Sequence 13, Appl
19	85	48.0	695	9	US-09-794-927-14	Sequence 14, Appl
20	85	48.0	695	9	US-09-795-847-14	Sequence 14, Appl
21	85	48.0	695	9	US-09-794-743-14	Sequence 14, Appl
22	85	48.0	695	9	US-09-794-748-14	Sequence 14, Appl
23	85	48.0	695	9	US-09-794-925-14	Sequence 14, Appl
24	85	48.0	695	9	US-09-681-442-14	Sequence 14, Appl
25	85	48.0	695	10	US-09-869-414-14	Sequence 14, Appl
26	85	48.0	695	10	US-09-548-366-14	Sequence 14, Appl
27	85	48.0	695	12	US-10-652-927-14	Sequence 14, Appl
28	85	48.0	695	12	US-10-652-830-14	Sequence 14, Appl
29	85	48.0	697	9	US-09-794-927-20	Sequence 20, Appl
30	85	48.0	697	9	US-09-795-847-20	Sequence 20, Appl
31	85	48.0	697	9	US-09-794-743-20	Sequence 20, Appl
32	85	48.0	697	9	US-09-794-748-20	Sequence 20, Appl
33	85	48.0	697	9	US-09-794-925-20	Sequence 20, Appl
34	85	48.0	697	9	US-09-681-442-20	Sequence 20, Appl
35	85	48.0	697	10	US-09-869-414-20	Sequence 20, Appl
36	85	48.0	697	10	US-09-548-366-20	Sequence 20, Appl
37	85	48.0	697	12	US-10-652-927-20	Sequence 20, Appl
38	85	48.0	697	12	US-10-652-830-20	Sequence 20, Appl
39	84	47.5	42	14	US-10-217-584-11	Sequence 11, Appl
40	84	47.5	43	9	US-09-972-475-3	Sequence 3, Appli
41	84	47.5	43	15	US-10-463-729-3	Sequence 3, Appli
42	83	46.9	16	9	US-09-155-076-2	Sequence 2, Appli
43	83	46.9	16	12	US-10-423-047-2	Sequence 2, Appli
44	83	46.9	16	15	US-10-411-544-22	Sequence 22, Appl
45	83	46.9	17	9	US-09-992-800-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-865-294-73
; Sequence 73, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Measles virus
US-09-865-294-73

Query Match 100.0%; Score 177; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34
              ||||||||||||||||||||||||||||||||||
Db          1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34
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RESULT 2
US-09-865-294-75
; Sequence 75, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294

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;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
;    LENGTH: 34
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-75

  Query Match             92.1%;  Score 163;  DB 10;  Length 34;
  Best Local Similarity   91.2%;  Pred. No. 1.4e-16;
  Matches   31;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34
              |||||||||||||||||||:||||||||:|| |||
Db          1 DAEFRHDSGYEVHHKISISEIKGVIVHKIEGILF 34


RESULT 3
US-09-865-294-74
; Sequence 74, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
;    LENGTH: 48
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-74

  Query Match             90.4%;  Score 160;  DB 10;  Length 48;
  Best Local Similarity   70.8%;  Pred. No. 5.7e-16;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels   14;  Gaps    1;

Qy          1 DAEFRHDSGYEVHH--------------KISITEIKGVIVHRIETILF 34
              ||||||||||||||              ||||||||||||||||||||
Db          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48


RESULT 4
US-09-865-294-76
; Sequence 76, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
;    LENGTH: 34
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-76

  Query Match             88.1%;  Score 156;  DB 10;  Length 34;
  Best Local Similarity   91.2%;  Pred. No. 1.4e-15;
  Matches   31;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34
              ||||||||||||||||||||: ||| |||||||
Db          1 DAEFRHDSGYEVHHKISITEIRTVIVTRIETILF 34


RESULT 5
US-09-865-294-72
; Sequence 72, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
;    LENGTH: 32
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-72

  Query Match             84.7%;  Score 150;  DB 10;  Length 32;
  Best Local Similarity   94.1%;  Pred. No. 1e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34
              |||||||||||| ||||||||||||||||||
Db          1 DAEFRHDSGYEV--KISITEIKGVIVHRIETILF 32


RESULT 6
US-09-865-294-71
; Sequence 71, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
;    LENGTH: 30
;    TYPE: PRT
;    ORGANISM: Measles virus
US-09-865-294-71

  Query Match             79.1%;  Score 140;  DB 10;  Length 30;
  Best Local Similarity   88.2%;  Pred. No. 2.7e-13;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    4;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34
              ||||||||||     ||||||||||||||||||||
Db          1 DAEFRHDSGY----KISITEIKGVIVHRIETILF 30


RESULT 7
US-09-865-294-51
; Sequence 51, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Chang Yi
;  TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
;  TITLE OF INVENTION:  prevention and treatment of Alzheimer's Disease
;  FILE REFERENCE: 1151-4167
;  CURRENT APPLICATION NUMBER: US/09/865,294
;  CURRENT FILING DATE:  2001-05-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
;    LENGTH: 19
;    TYPE: PRT
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;   ORGANISM: Measles virus
US-09-865-294-51

  Query Match             50.8%;  Score 90;  DB 10;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 ISITEIKGVIVHRIETILF 34
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 8
US-10-076-674-6
; Sequence 6, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/076,674
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-6

  Query Match             50.8%;  Score 90;  DB 14;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 ISITEIKGVIVHRIETILF 34
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 9
US-10-355-161A-6
; Sequence 6, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-6

  Query Match             50.8%;  Score 90;  DB 15;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 ISITEIKGVIVHRIETILF 34
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 10
US-10-076-674-11
; Sequence 11, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/076,674
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 45
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-11

  Query Match             50.8%;  Score 90;  DB 14;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 ISITEIKGVIVHRIETILF 34
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 11
US-10-355-161A-11
; Sequence 11, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 45
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-11

  Query Match             50.8%;  Score 90;  DB 15;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 ISITEIKGVIVHRIETILF 34
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 12
US-10-076-674-4
; Sequence 4, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
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;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/076,674
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 50
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-4

  Query Match             50.8%;  Score 90;  DB 14;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 ISITEIKGVIVHRIETILF 34
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 13
US-10-355-161A-4
; Sequence 4, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
;  APPLICANT: Sokoll, Kenneth K.
;  TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
;  FILE REFERENCE: Immunogen Delivery System
;  CURRENT APPLICATION NUMBER: US/10/355,161A
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 10/076674
;  PRIOR FILING DATE: 2002-02-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 50
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-4

  Query Match             50.8%;  Score 90;  DB 15;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 ISITEIKGVIVHRIETILF 34
              |||||||||||||||||||
Db          1 ISITEIKGVIVHRIETILF 19


RESULT 14
US-09-972-475-15
; Sequence 15, Application US/09972475
; Patent No. US20020098173A1
;   GENERAL INFORMATION:
;        APPLICANT: Findeis, Mark A. et al.
;        TITLE OF INVENTION: Modulators of Amyloid Aggregation
;        NUMBER OF SEQUENCES: 45
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: LAHIVE & COCKFIELD, LLP
;             STREET: 28 State Street
;             CITY: Boston
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02109-1875
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/972,475
;             FILING DATE: 04-Oct-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/617,267
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: USSN 08/475,579
;             FILING DATE: 07-JUN-1995
;             APPLICATION NUMBER: USSN 08/548,998
;             FILING DATE: 27-OCT-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: DeConti, Giulio A.
;             REGISTRATION NUMBER: 31,503
;             REFERENCE/DOCKET NUMBER: PPI-002CP2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617)227-7400
;             TELEFAX: (617)227-5941
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 35 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        FRAGMENT TYPE: internal
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-972-475-15

  Query Match             50.6%;  Score 89.5;  DB 9;  Length 35;
  Best Local Similarity   66.7%;  Pred. No. 7.6e-06;
  Matches   18;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 DAEFRHDSGYEVHH-KISITEIKGVIV 26
              |||||||||||||| |:     || |:
Db          1 DAEFRHDSGYEVHHQKLVFFSNKGAII 27


RESULT 15
US-10-463-729-15
; Sequence 15, Application US/10463729
; Publication No. US20040005307A1
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Modulators of Amyloid Aggregation
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/463,729
;      FILING DATE:  17-JUNE-2003
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/617,267C
;      FILING DATE:  14-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/548,998
;      FILING DATE:  27-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PPI-002CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-10-463-729-15

  Query Match             50.6%;  Score 89.5;  DB 15;  Length 35;
  Best Local Similarity   66.7%;  Pred. No. 7.6e-06;
  Matches   18;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 DAEFRHDSGYEVHH-KISITEIKGVIV 26
              |||||||||||||| |:     || |:
Db          1 DAEFRHDSGYEVHHQKLVFFSNKGAII 27


Search completed: June 18, 2004, 20:23:47
Job time : 38.3804 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:45 ; Search time 10.2209 Seconds
(without alignments)
319.984 Million cell updates/sec

Title: US-09-865-294A-73
Perfect score: 177
Sequence: 1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	46.9	42	2	PN0512	beta-amyloid prote
2	83	46.9	57	2	E60045	Alzheimer's diseas
3	83	46.9	57	2	F60045	Alzheimer's diseas
4	83	46.9	57	2	G60045	Alzheimer's diseas
5	83	46.9	57	2	D60045	Alzheimer's diseas
6	83	46.9	57	2	A60045	Alzheimer's diseas
7	83	46.9	57	2	B60045	Alzheimer's diseas
8	83	46.9	82	2	PQ0438	Alzheimer's diseas
9	83	46.9	695	1	A49795	Alzheimer's diseas
10	83	46.9	770	1	QRHUA4	Alzheimer's diseas
11	68	38.4	747	2	JH0773	Alzheimer's diseas
12	64	36.2	33	2	S23094	beta-amyloid prote
13	64	36.2	546	1	VGNZRL	cell fusion glycop
14	64	36.2	695	2	A27485	Alzheimer's diseas
15	64	36.2	695	2	S00550	Alzheimer's diseas
16	61	34.5	546	2	S47300	gene F protein - r
17	60	33.9	546	1	VGNZRK	cell fusion glycop
18	60	33.9	546	2	S55386	cell fusion protei
19	60	33.9	546	2	S47305	gene F protein - r
20	59	33.3	542	2	JQ2223	cell fusion protei
21	59	33.3	552	2	S47034	cell fusion protei
22	59	33.3	662	1	VGNZCD	cell fusion glycop
23	59	33.3	662	2	S21382	cell fusion protei
24	58	32.8	282	2	PQ0376	cell fusion glycop
25	58	32.8	282	2	PQ0388	cell fusion glycop
26	58	32.8	534	1	JU0274	cell fusion glycop
27	58	32.8	550	1	E48556	cell fusion glycop
28	58	32.8	553	1	VGNZMV	cell fusion glycop
29	58	32.8	631	1	VGNZPD	cell fusion glycop
30	58	32.8	631	1	A48346	cell fusion glycop
31	57.5	32.5	356	2	D96537	hypothetical prote
32	54.5	30.8	236	2	A90190	hypothetical prote
33	52	29.4	220	2	T00801	probable synaptobr
34	52	29.4	229	2	F86180	hypothetical prote
35	51.5	29.1	539	2	T39150	probable heat shoc
36	51	28.8	239	2	T34305	hypothetical prote
37	51	28.8	240	2	T47589	synaptobrevin-like
38	51	28.8	854	2	D83077	ClpB protein PA454
39	50.5	28.5	427	2	S38002	hypothetical prote
40	50.5	28.5	503	2	AB1933	hypothetical prote
41	50	28.2	605	2	G70409	high affinity sulf
42	49.5	28.0	367	2	C96537	hypothetical prote
43	49.5	28.0	615	2	A82025	probable outer mem
44	49.5	28.0	635	2	G81003	conserved hypothet
45	49.5	28.0	4563	1	LPHUB	apolipoprotein B-1

ALIGNMENTS

RESULT 1
PN0512
beta-amyloid protein - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PN0512
R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno,
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragm
A;Reference number: PN0512; MUID:93290653; PMID:7685598
A;Accession: PN0512
A;Molecule type: protein
A;Residues: 1-42 <SHI>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid

Query Match 46.9%; Score 83; DB 2; Length 42;
Best Local Similarity 93.3%; Pred. No. 6e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||||:
Db          1 DAEFRHDSGYEVHHQ 15
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RESULT 2
E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C;Species: Ovis sp. (sheep)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: E60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: E60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56130
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 46.9%; Score 83; DB 2; Length 57;
Best Local Similarity 93.3%; Pred. No. 8.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||||:
Db          6 DAEFRHDSGYEVHHQ 20
```

RESULT 3

F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: F60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: F60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 46.9%; Score 83; DB 2; Length 57;
Best Local Similarity 93.3%; Pred. No. 8.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHK 15
||||||||||||||:
Db 6 DAEFRHDSGYEVHHQ 20

RESULT 4
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: G60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: G60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56126
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 46.9%; Score 83; DB 2; Length 57;
Best Local Similarity 93.3%; Pred. No. 8.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHK 15
||||||||||||||:
Db 6 DAEFRHDSGYEVHHQ 20

RESULT 5
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: D60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: D60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56124
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 46.9%; Score 83; DB 2; Length 57;
Best Local Similarity 93.3%; Pred. No. 8.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHK 15
||||||||||||||:
Db 6 DAEFRHDSGYEVHHQ 20

RESULT 6
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: A60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: A60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56125
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 46.9%; Score 83; DB 2; Length 57;
Best Local Similarity 93.3%; Pred. No. 8.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHK 15
||||||||||||||:
Db 6 DAEFRHDSGYEVHHQ 20

RESULT 7
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C;Species: Ursus maritimus (polar bear)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: B60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: B60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 46.9%; Score 83; DB 2; Length 57;
Best Local Similarity 93.3%; Pred. No. 8.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHK 15
||||||||||||||:
Db 6 DAEFRHDSGYEVHHQ 20

RESULT 8
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: PQ0438; C60045
R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurso
A;Reference number: PQ0438; MUID:93075180; PMID:1445331
A;Accession: PQ0438
A;Molecule type: DNA
A;Residues: 1-82 <DAV>
A;Cross-references: GB:M83558; GB:M83657
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog

A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: C60045
A;Molecule type: mRNA
A;Residues: 12-68 <JOH>
A;Cross-references: EMBL:X56129
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 46.9%; Score 83; DB 2; Length 82;
Best Local Similarity 93.3%; Pred. No. 0.00013;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHK 15
||||||||||||||:
Db 17 DAEFRHDSGYEVHHQ 31

RESULT 9
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49795
R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a p
A;Reference number: A49795; MUID:91273117; PMID:1905108
A;Accession: A49795
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-695 <POD>
A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing

Query Match 46.9%; Score 83; DB 1; Length 695;
Best Local Similarity 93.3%; Pred. No. 0.0013;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHK 15
||||||||||||||:
Db 597 DAEFRHDSGYEVHHQ 611

RESULT 10
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibi
N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44
4668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S3
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288,'V',365-770 <LEM1>
A;Cross-references: EMBL:X13466
A;Note: alternative splice form APP(695)
R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A;Note: alternative splice form APP(695)
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prot
A;Reference number: A32277; MUID:89165870; PMID:2538123
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAF>
A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similari
A;Reference number: A33260; MUID:89392030; PMID:2675837
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMI
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMI
A;Molecule type: DNA
A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duin
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheime
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 689-716,'F',718-737 <MUR>
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692,'G',694-718 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA

A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288,'V',365-770 <KAN>
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756,'S',758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344,'I',365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344,'I',365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashto
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288,'V',365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 60
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 6
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K

  Query Match 46.9%; Score 83; DB 1; Length 770;
  Best Local Similarity 93.3%; Pred. No. 0.0015;
  Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHK 15
||||||||||||||:
Db 672 DAEFRHDSGYEVHHQ 686

RESULT 11
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match 38.4%; Score 68; DB 2; Length 747;
  Best Local Similarity 66.7%; Pred. No. 0.19;
  Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHK 15
|:|:|||: |||||:
Db 649 DSEYRHDTAYEVHHQ 663

RESULT 12
S23094
beta-amyloid protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C;Accession: S23094
R;Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
A;Reference number: S23094; MUID:92316198; PMID:1618299
A;Accession: S23094
A;Molecule type: protein
A;Residues: 1-33 <KOJ>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

Query Match 36.2%; Score 64; DB 2; Length 33;
Best Local Similarity 73.3%; Pred. No. 0.022;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHK 15
||||.||||:||.|:
Db 6 DAEFGHDSGFEVRHQ 20

RESULT 13
VGNZRL
cell fusion glycoprotein precursor - rinderpest virus (strain L)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: rinderpest virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Accession: A28921
R;Tsukiyama, K.; Yoshikawa, Y.; Yamanouchi, K.
Virology 164, 523-530, 1988
A;Title: Fusion glycoprotein (F) of rinderpest virus: entire nucleotide sequence of the
A;Reference number: A28921; MUID:88219541; PMID:3285575
A;Accession: A28921
A;Molecule type: mRNA
A;Residues: 1-546 <TSU>
A;Cross-references: GB:M20870; NID:g333898; PIDN:AAA47399.1; PID:g333899
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-104/Product: cell fusion glycoprotein F2 #status predicted <FG2>
F;105-546/Product: cell fusion glycoprotein F1 #status predicted <FG1>
F;109-133/Domain: transmembrane #status predicted <TN1>
F;485-513/Domain: transmembrane #status predicted <TN2>
F;25,57,63/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.2%; Score 64; DB 1; Length 546;
Best Local Similarity 61.1%; Pred. No. 0.49;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 17 SITEIKGVIVHRIETILF 34
|::|||||||||:|:: :
Db 283 SLSEIKGVIVHRLESVSY 300

RESULT 14
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N;Alternate names: proteinase nexin II
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C;Accession: A27485; S19727; I49485
R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu
A;Reference number: A27485; MUID:88106489; PMID:3322280
A;Accession: A27485
A;Molecule type: mRNA
A;Residues: 1-695 <YAM>
A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A;Experimental source: brain
R;de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A;Reference number: S19727; MUID:92096458; PMID:1756177
A;Accession: S19727
A;Molecule type: mRNA
A;Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695 <STR>
A;Cross-references: EMBL:X59379
R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the Alzheimer'
A;Reference number: I49485; MUID:92209998; PMID:1555768
A;Accession: I49485
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
A;Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C;Genetics:
A;Map position: 16C3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 36.2%; Score 64; DB 2; Length 695;
Best Local Similarity 73.3%; Pred. No. 0.64;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHK 15
||||.||||:||.|:
Db 597 DAEFGHDSGFEVRHQ 611

RESULT 15
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brai
A;Reference number: S00550; MUID:88312583; PMID:2900758
A;Accession: S00550
A;Molecule type: mRNA
A;Residues: 1-695 <SHI>
A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A;Reference number: A41245; MUID:88264430; PMID:2968652
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627; PMID:7913895
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brai
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is ch
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TMM>

Query Match 36.2%; Score 64; DB 2; Length 695;

Best Local Similarity 73.3%; Pred. No. 0.64;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 DAEFRHDSGYEVHHK 15
              |||| |||| :|| |:
Db        597 DAEFGHDSGFEVRHQ 611
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Search completed: June 18, 2004, 20:03:31
Job time : 11.2209 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:55 ; Search time 6.67485 Seconds
(without alignments)
265.232 Million cell updates/sec

Title: US-09-865-294A-73
Perfect score: 177
Sequence: 1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	46.9	57	1	A4_URSMA	Q29149 ursus marit
2	83	46.9	58	1	A4_CANFA	Q28280 canis famil
3	83	46.9	58	1	A4_RABIT	Q28748 oryctolagus
4	83	46.9	58	1	A4_SHEEP	Q28757 ovis aries
5	83	46.9	59	1	A4_BOVIN	Q28053 bos taurus
6	83	46.9	751	1	A4_SAISC	Q95241 s amyloid b
7	83	46.9	770	1	A4_CAVPO	Q60495 c amyloid b
8	83	46.9	770	1	A4_HUMAN	P05067 h amyloid b
9	83	46.9	770	1	A4_MACFA	P53601 m amyloid b
10	83	46.9	770	1	A4_PIG	P79307 s amyloid b
11	64	36.2	546	1	VGLF_RINDL	P10864 rinderpest
12	64	36.2	770	1	A4_MOUSE	P12023 m amyloid b
13	64	36.2	770	1	A4_RAT	P08592 r amyloid b
14	61	34.5	546	1	VGLF_RINDB	P41360 rinderpest
15	60	33.9	546	1	VGLF_RINDR	P41356 rinderpest
16	59	33.3	662	1	VGLF_CDVO	P12569 canine dist
17	58	32.8	534	1	VGLF_MEASY	P26032 measles vir
18	58	32.8	550	1	VGLF_MEASA	P35973 measles vir
19	58	32.8	550	1	VGLF_MEASE	P08300 measles vir
20	58	32.8	631	1	VGLF_PHODV	P28886 phocine dis
21	57.5	32.5	356	1	BCA6_ARATH	Q9lpm9 arabidopsis
22	54	30.5	546	1	VGLF_RINDK	P12574 rinderpest
23	52	29.4	220	1	V725_ARATH	O48850 arabidopsis
24	52	29.4	229	1	V726_ARATH	Q9mas5 arabidopsis
25	51.5	29.1	539	1	PRR1_SCHPO	O14283 schizosacch
26	51	28.8	207	1	CCPL_CAEEL	P53806 caenorhabdi
27	51	28.8	240	1	V727_ARATH	Q9m376 arabidopsis
28	50.5	28.5	427	1	BBP2_YEAST	P36049 saccharomyc
29	50	28.2	529	1	VGLF_MEASI	P26031 measles vir
30	49.5	28.0	208	1	PSD_METMA	Q8px20 methanosarc
31	49.5	28.0	367	1	BCA7_ARATH	Q9lpm8 arabidopsis
32	49.5	28.0	4563	1	APB_HUMAN	P04114 homo sapien
33	49	27.7	231	1	HGXR_PLAFK	P07833 plasmodium
34	49	27.7	347	1	6OMT_COPJA	Q9lel6 coptis japo
35	49	27.7	726	1	TRF_BLADI	Q02942 blaberus di
36	49	27.7	925	1	W70T_HUMAN	P57737 homo sapien
37	48.5	27.4	284	1	POLG_PVYYO	P11897 potato viru
38	48.5	27.4	327	1	POLG_PVYCH	P21294 potato viru
39	48	27.1	219	1	V721_ARATH	Q9ztw3 arabidopsis
40	48	27.1	221	1	V722_ARATH	P47192 arabidopsis
41	48	27.1	231	1	HGXR_PLAFG	P20035 plasmodium
42	48	27.1	449	1	TIG_RALSO	Q8xyp8 ralstonia s
43	48	27.1	810	1	CLPC_BACSU	P37571 bacillus su
44	48	27.1	848	1	CLPC_MYCLE	P24428 mycobacteri
45	48	27.1	848	1	CLPC_MYCTU	O06286 mycobacteri

ALIGNMENTS

RESULT 1
A4_URSMA
ID A4_URSMA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ursus maritimus (Polar bear) (Thalarctos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC --

CC --
DR EMBL; X56128; CAA39593.1; -.
DR PIR; B60045; B60045.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 46.9%; Score 83; DB 1; Length 57;
Best Local Similarity 93.3%; Pred. No. 3.7e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 DAEFRHDSGYEVHHK 15
              ||||||||||||||:
Db          6 DAEFRHDSGYEVHHQ 20


RESULT 2
A4_CANFA
ID   A4_CANFA       STANDARD;      PRT;    58 AA.
AC   Q28280;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56125; CAA39590.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     58       POTENTIAL.
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6285 MW;  8469D488A2E12DFA CRC64;

  Query Match             46.9%;  Score 83;  DB 1;  Length 58;
  Best Local Similarity   93.3%;  Pred. No. 3.8e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              ||||||||||||||:
Db          7 DAEFRHDSGYEVHHQ 21


RESULT 3
A4_RABIT
ID   A4_RABIT       STANDARD;      PRT;    58 AA.
AC   Q28748;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56129; CAA39594.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   DOMAIN       58    >58       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6300 MW;  F434209D88EBA82D CRC64;

  Query Match             46.9%;  Score 83;  DB 1;  Length 58;
  Best Local Similarity   93.3%;  Pred. No. 3.8e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              ||||||||||||||:
Db          6 DAEFRHDSGYEVHHQ 20


RESULT 4
A4_SHEEP
ID   A4_SHEEP       STANDARD;      PRT;    58 AA.
AC   Q28757;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
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RC   TISSUE=Heart;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56130; CAA39595.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   DOMAIN       58    >58       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6300 MW;  F434209D88EBA82D CRC64;

  Query Match             46.9%;  Score 83;  DB 1;  Length 58;
  Best Local Similarity   93.3%;  Pred. No. 3.8e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||||:
Db          6 DAEFRHDSGYEVHHQ 20


RESULT 5
A4_BOVIN
ID   A4_BOVIN       STANDARD;      PRT;    59 AA.
AC   Q28053;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56124; CAA39589.1; -.
DR   EMBL; X56126; CAA39591.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     58       POTENTIAL.
FT   DOMAIN       59    >59       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      59     59
SQ   SEQUENCE   59 AA;  6414 MW;  F43469D488A2E12D CRC64;

  Query Match             46.9%;  Score 83;  DB 1;  Length 59;
  Best Local Similarity   93.3%;  Pred. No. 3.9e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||||:
Db          7 DAEFRHDSGYEVHHQ 21


RESULT 6
A4_SAISC
ID   A4_SAISC       STANDARD;      PRT;    751 AA.
AC   Q95241;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
DE   APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
DE   Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
DE   CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Liver;
RX   MEDLINE=96108492; PubMed=8532114;
RA   Levy E., Amorim A., Prangione B., Walker L.C.;
RT   "Beta-amyloid precursor protein gene in squirrel monkeys with
RT   cerebral amyloid angiopathy.";
RL   Neurobiol. Aging 16:805-808(1995).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(0) alpha ATPase activity (By similarity).
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CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=Q95241-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q95241-2; Sequence=Not described;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; S81024; AAD14347.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Amyloid; Alternative splicing.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    751       A4 PROTEIN.
FT   CHAIN        18    668       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    652       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       653    751       C99 (POTENTIAL).
FT   CHAIN       653    694       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN       653    692       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN       669    751       C83 (POTENTIAL).
FT   CHAIN       669    694       P3(42) (POTENTIAL).
FT   CHAIN       669    692       P3(40) (POTENTIAL).
FT   CHAIN       693    751       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN       695    751       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN       702    751       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN       721    751       C31 (POTENTIAL).
FT   DOMAIN       18    680       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    681    704       POTENTIAL.
FT   DOMAIN      705    751       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      316    344       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      363    428       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      504    521       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      713    732       INTERACTION WITH G(O)-ALPHA
FT                                (BY SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND.
FT   SITE        652    653       CLEAVAGE (BY BETA-SECRETASE)
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FT                                   (BY SIMILARITY).
FT   SITE        653    654          CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        668    669          CLEAVAGE (BY ALPHA-SECRETASE)
FT                                   (BY SIMILARITY).
FT   SITE        685    685          INVOLVED IN FREE RADICAL PROPAGATION
FT                                   (BY SIMILARITY).
FT   SITE        687    687          INVOLVED IN OXIDATIVE REACTIONS
FT                                   (BY SIMILARITY).
FT   SITE        692    693          CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                   (BY SIMILARITY).
FT   SITE        694    695          CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                   (BY SIMILARITY).
FT   SITE        701    702          CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                   (BY SIMILARITY).
FT   SITE        705    715          BASOLATERAL SORTING SIGNAL
FT                                   (BY SIMILARITY).
FT   SITE        720    721          CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT                                   (BY SIMILARITY).
FT   SITE        738    741          ENDOCYTOSIS SIGNAL.
FT   SITE        740    743          NPXY MOTIF.

  Query Match             46.9%;  Score 83;  DB 1;  Length 751;
  Best Local Similarity   93.3%;  Pred. No. 0.00058;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||:
Db        653 DAEFRHDSGYEVHHQ 667


RESULT 7
A4_CAVPO
ID   A4_CAVPO       STANDARD;      PRT;   770 AA.
AC   Q60495; Q60496;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
DE   protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
DE   P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE   CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
GN   APP.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Liver;
RX   MEDLINE=97236426; PubMed=9116031;
RA   Beck M., Mueller D., Bigl V.;
RT   "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT   alternative splicing.";
RL   Biochim. Biophys. Acta 1351:17-21(1997).
RN   [2]
RP   INTERACTION OF BETA-APP40 WITH APOE.
RX   MEDLINE=98007700; PubMed=9349544;
RA   Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
RA   Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
RT   "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
RT   cerebral capillary sequestration and blood-brain barrier transport of
RT   circulating Alzheimer's amyloid beta.";
RL   J. Neurochem. 69:1995-2004(1997).
RN   [3]
RP   PROCESSING.
RX   MEDLINE=20084499; PubMed=10619481;
RA   Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA   Bigl V.;
RT   "Guinea-pig primary cell cultures provide a model to study expression
RT   and amyloidogenic processing of endogenous amyloid precursor
RT   protein.";
RL   Neuroscience 95:243-254(2000).
RN   [4]
RP   GAMMA-SECRETASE PROCESSING.
RX   MEDLINE=20576391; PubMed=11035007;
RA   Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA   Ziani-Cherif C., Onstead L., Sambamurti K.;
RT   "A novel gamma -secretase assay based on detection of the putative
RT   C-terminal fragment-gamma of amyloid beta protein precursor.";
RL   J. Biol. Chem. 276:481-487(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC       and apoliproteins E and J in the CSF and to HDL particles in
CC       plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) and DDB1 (By similarity).
CC       Associates with microtubules in the presence of ATP and in a
CC       kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC       all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC       ApoE3 appears to be the preferred amyloid binding isoform, while
CC       the apoE4 isoform-beta-APP40 complex is capable of being
CC       transported across the blood-brain barrier.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated pits
CC       (By similarity). During maturation, the immature APP (N-
CC       glycosylated in the endoplasmic reticulum) moves to the Golgi
CC       complex where complete maturation occurs (O-glycosylated and
CC       sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC       APP is released into the extracellular space and the C-terminal is
CC       internalized to endosomes and lysosomes (By similarity). Some APP
CC       accumulates in secretory transport vesicles leaving the late Golgi
CC       compartment and returns to the cell surface (By similarity). APP
CC       sorts to the basolateral surface in epithelial cells (By
CC       similatity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms, missing exons 7,8 and 15, seem to
CC         exist. The L-isoforms, missing exon 15, are referred to as
CC         appicans;
CC       Name=APP770;
CC         IsoId=Q60495-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
CC   -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC       brain. The longer isoforms containing the BPTI domain are
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CC       predominantly expressed in peripheral organs such as muscle and
CC       liver.
CC   -!- INDUCTION: Increased levels during neuronal differentiation.
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells.
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue (By similarity). The NPXY site is also involved in
CC       clathrin-mediated endocytosis.
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC       gamma-secretase yields P3 peptides. This is the major secretory
CC       pathway and is nonamyloidogenic. Alternatively,
CC       presenilin/nicastrin-mediated gamma-secretase processing of CTF-
CC       beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC       and amyloid-beta 42 (Abeta42), major components of amyloid
CC       plaques, and the corresponding cytotoxic C-terminal fragments
CC       (CTFs).
CC   -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC       apoptosis (By similarity).
CC   -!- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
CC       the L-APP isoforms produces the APP proteoglycan core proteins,
CC       the appicans (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific (By similarity).
CC       Phosphorylation can affect APP processing, neuronal
CC       differentiation and interaction with other proteins.
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X97631; CAA66230.1; -.
DR   EMBL; X99198; CAA67589.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (BY SIMILARITY).
FT   CHAIN        18    671       SOLUBLE APP-BETA (BY SIMILARITY).
FT   CHAIN       672    770       CTF-ALPHA (BY SIMILARITY).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688    770       CTF-BETA (BY SIMILARITY).
FT   CHAIN       688    713       P3(42) (BY SIMILARITY).
FT   CHAIN       688    711       P3(40) (BY SIMILARITY).
FT   CHAIN       712    770       GAMMA-CTF(59) (BY SIMILARITY).
FT   CHAIN       714    770       GAMMA-CTF(57) (BY SIMILARITY).

  Query Match             46.9%;  Score 83;  DB 1;  Length 770;
  Best Local Similarity   93.3%;  Pred. No. 0.0006;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||||:
Db        672 DAEFRHDSGYEVHHQ 686


RESULT 8
A4_HUMAN
ID   A4_HUMAN        STANDARD;      PRT;   770 AA.
AC   P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
AC   Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCC8; Q9UCD1; Q9UQ58;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE   nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE   alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE   (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE   P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE   (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE   secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE   (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE   (Amyloid intracellular domain 50) (AID(50)); C31].
GN   APP OR A4 OR AD1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=87144572; PubMed=2881207;
RA   Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA   Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT   "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT   cell-surface receptor.";
RL   Nature 325:733-736(1987).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM APP751).
RC   TISSUE=Brain;
RX   MEDLINE=88122639; PubMed=2893289;
RA   Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA   Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA   Cordell B.;
RT   "A new A4 amyloid mRNA contains a domain homologous to serine
RT   proteinase inhibitors.";
RL   Nature 331:525-527(1988).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RX   MEDLINE=89128427; PubMed=2783775;
RA   Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA   Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT   "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT   is encoded by 16 exons.";
RL   Nucleic Acids Res. 17:517-522(1989).
```

RN [4]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";
RL Gene 87:257-263(1990).
RN [5]
RP ERRATUM, AND REVISIONS.
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RL Gene 102:291-292(1991).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
RC TISSUE=Leukocyte;
RX MEDLINE=92268136; PubMed=1587857;
RA Koenig G., Moenning U., Czech C., Prior R., Banati R.,
RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
RT "Identification and differential expression of a novel alternative
RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
RT leukocytes and brain microglial cells.";
RL J. Biol. Chem. 267:10804-10809(1992).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM APP639).
RC TISSUE=Brain;
RX MEDLINE=22744650; PubMed=12859342;
RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
RT "Identification of a novel alternative splicing isoform of human
RT amyloid precursor protein gene, APP639.";
RL Eur. J. Neurosci. 18:102-108(2003).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM APP305).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [11]
RP ERRATUM, AND REVISIONS.
RA Mita S., Sadlock J., Herbert J., Schon E.A.;
RL Nucleic Acids Res. 16:11402-11402(1988).
RN [12]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE=89165870; PubMed=2538123;
RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
RT "Characterization of the 5'-end region and the first two exons of the
RT beta-protein precursor gene.";
RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
RN [13]
RP SEQUENCE OF 18-50.
RC TISSUE=Fibroblast;
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [14]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=89346754; PubMed=2569763;
RA de Sauvage F., Octave J.N.;
RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT secreted protein.";
RL Science 245:651-653(1989).
RN [15]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [16]
RP SEQUENCE OF 286-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [17]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [18]
RP SEQUENCE OF 507-770 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [19]
RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX MEDLINE=96139497; PubMed=8576160;
RA Beher D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [20]
RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717
RP AND AD GLY-717.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzcwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
RN [21]
RP SEQUENCE OF 656-737 FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;

```
RA   Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA   Little S.P.;
RT   "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT   similarity to soybean trypsin inhibitor.";
RL   Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN   [22]

  Query Match             46.9%;  Score 83;  DB 1;  Length 770;
  Best Local Similarity   93.3%;  Pred. No. 0.0006;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||||:
Db        672 DAEFRHDSGYEVHHQ 686


RESULT 9
A4_MACFA
ID   A4_MACFA        STANDARD;       PRT;   770 AA.
AC   P53601; Q95KN7;
DT   01-OCT-1996 (Rel. 34, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC   TISSUE=Cerebellum;
RX   MEDLINE=91273117; PubMed=1905108;
RA   Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT   "Homology of the amyloid beta protein precursor in monkey and human
RT   supports a primate model for beta amyloidosis in Alzheimer's
RT   disease.";
RL   Am. J. Pathol. 138:1423-1435(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=P53601-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
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CC   ----------------------------------------------------------------------
DR   EMBL; M58727; AAA36829.1; -.
DR   EMBL; M58726; AAA36828.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672    770       C99 (POTENTIAL).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN       688    770       C83 (POTENTIAL).
FT   CHAIN       688    713       P3(42) (POTENTIAL).
FT   CHAIN       688    711       P3(40) (POTENTIAL).
FT   CHAIN       712    770       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN       714    770       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN       721    770       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN       740    770       C31 (POTENTIAL).
FT   DOMAIN       18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    700    723       POTENTIAL.
FT   DOMAIN      724    770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      391    423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      491    522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      523    540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      732    751       INTERACTION WITH G(O)-ALPHA
FT                                (BY SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND (BY SIMILARITY).
FT   SITE        671    672       CLEAVAGE (BY BETA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        672    673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        687    688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        704    704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                                (BY SIMILARITY).
FT   SITE        706    706       INVOLVED IN OXIDATIVE REACTIONS
FT                                (BY SIMILARITY).
FT   SITE        711    712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                (BY SIMILARITY).
FT   SITE        713    714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                (BY SIMILARITY).
FT   SITE        720    721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                (BY SIMILARITY).
FT   SITE        724    734       BASOLATERAL SORTING SIGNAL
FT                                (BY SIMILARITY).
FT   SITE        739    740       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
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  Query Match             46.9%;  Score 83;  DB 1;  Length 770;
  Best Local Similarity   93.3%;  Pred. No. 0.0006;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||||:
Db        672 DAEFRHDSGYEVHHQ 686


RESULT 10
A4_PIG
ID   A4_PIG          STANDARD;      PRT;   770 AA.
AC   P79307; Q29023; Q9TUI0;
DT   01-NOV-1997 (Rel. 35, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura A., Takahashi T.;
RT   "Amyloid precursor protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-136 FROM N.A.
RC   TISSUE=Small intestine;
RA   Winteroe A.K., Fredholm M.;
RT   "Evaluation and characterization of a porcine small intestine cDNA
RT   library.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 667-723 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
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CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, PPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB032550; BAA84580.1; -.
DR   EMBL; Z84022; CAB06313.1; -.
DR   EMBL; X56127; CAA39592.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Amyloid.
FT   SIGNAL       1    17       BY SIMILARITY.
FT   CHAIN       18   770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN       18   687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN       18   671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN      672   770       C99 (BY SIMILARITY).
FT   CHAIN      672   713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN      672   711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN      688   770       C83 (BY SIMILARITY).
FT   CHAIN      688   713       P3(42) (BY SIMILARITY).
FT   CHAIN      688   711       P3(40) (BY SIMILARITY).
FT   CHAIN      712   770       GAMMA-CTF(59).
FT   CHAIN      714   770       GAMMA-CTF(57).
FT   CHAIN      721   770       GAMMA-CTF(50) (BY SIMILARITY).
FT   CHAIN      740   770       C31 (DURING APOPTOSIS) (BY SIMILARITY).
FT   DOMAIN      18   699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   700   723       POTENTIAL.
FT   DOMAIN     724   770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      96   110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     135   155       COPPER-BINDING (BY SIMILARITY).
FT   DOMAIN     181   188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN     291   341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN     391   423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     491   522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     523   540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN     732   751       INTERACTION WITH G(O)-ALPHA (BY
FT                              SIMILARITY).
FT   DOMAIN     230   260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN     274   280       POLY-THR.
FT   SITE       144   144       REQUIRED FOR COPPER(II) REDUCTION
FT                              (BY SIMILARITY).
FT   ACT_SITE   301   302       REACTIVE BOND (BY SIMILARITY).
FT   SITE       671   672       CLEAVAGE (BY BETA-SECRETASE)
FT                              (BY SIMILARITY).
FT   SITE       672   673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE       687   688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                              (BY SIMILARITY).
FT   SITE       704   704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                              (BY SIMILARITY).
FT   SITE       706   706       INVOLVED IN OXIDATIVE REACTIONS
FT                              (BY SIMILARITY).
FT   SITE       711   712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                              (BY SIMILARITY).
FT   SITE       713   714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                              (BY SIMILARITY).
FT   SITE       720   721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)

  Query Match             46.9%;  Score 83;  DB 1;  Length 770;
  Best Local Similarity   93.3%;  Pred. No. 0.0006;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              ||||||||||||||:
Db        672 DAEFRHDSGYEVHHQ 686
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RESULT 11
VGLF_RINDL
ID   VGLF_RINDL     STANDARD;      PRT;   546 AA.
AC   P10864;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Rinderpest virus (strain L) (RDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11243;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88219541; PubMed=3285575;
RA   Tsukiyama K., Yoshikawa Y., Yamanouchi K.;
RT   "Fusion glycoprotein (F) of rinderpest virus: entire nucleotide
RT   sequence of the F mRNA, and several features of the F protein.";
RL   Virology 164:523-530(1988).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M20870; AAA47399.1; -.
DR   PIR; A28921; VGNZRL.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    546       FUSION GLYCOPROTEIN F0.
FT   CHAIN        20    108       F2 PROTEIN.
FT   CHAIN       109    546       F1 PROTEIN.
FT   DOMAIN      104    108       ARG/LYS-RICH (BASIC).
FT   TRANSMEM    109    133       POTENTIAL.
FT   TRANSMEM    484    513       POTENTIAL.
FT   DOMAIN      514    517       ARG/LYS-RICH (BASIC).
FT   DISULFID     64    191       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD     25     25       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     57     57       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     63     63       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   546 AA;  58911 MW;  985029418F28FFB5 CRC64;

  Query Match             36.2%;  Score 64;  DB 1;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 0.21;
  Matches   11;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         17 SITEIKGVIVHRIETILF 34
              |::|||||||||:|:: :
Db        283 SLSEIKGVIVHRLESVSY 300


RESULT 12
A4_MOUSE
ID   A4_MOUSE       STANDARD;      PRT;   770 AA.
AC   P12023; P97487; P97942; Q99K32;
DT   01-OCT-1989 (Rel. 12, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:
DE   Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
DE   (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
DE   40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
DE   C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE   (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
DE   (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
DE   (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
DE   50) (AID(50)); C31].
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88106489; PubMed=3322280;
RA   Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT   "Complementary DNA for the mouse homolog of the human amyloid beta
RT   protein precursor.";
RL   Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN   [2]
RP   REVISIONS.
RA   Yamada T.;
RL   Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=BALB/c; TISSUE=Brain;
RX   MEDLINE=92096458; PubMed=1756177;
RA   de Strooper B., van Leuven F., van den Berghe H.;
RT   "The amyloid beta protein precursor or proteinase nexin II from mouse
RT   is closer related to its human homolog than previously reported.";
RL   Biochim. Biophys. Acta 1129:141-143(1991).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=SAMP8; TISSUE=Hippocampus;
RX   MEDLINE=21130647; PubMed=11235921;
RA   Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
RA   Alvarez J., Morley J.E.;
RT   "Molecular cloning, expression, and regulation of hippocampal amyloid
RT   precursor protein of senescence accelerated mouse (SAMP8).";
RL   Biochem. Cell Biol. 79:57-67(2001).
RN   [5]
RP   SEQUENCE OF 1-19 FROM N.A.
RX   MEDLINE=92209998; PubMed=1555768;
RA   Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA   Sakai Y.;
RT   "Positive and negative regulatory elements for the expression of the
RT   Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL   Gene 112:189-195(1992).
RN   [6]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
RC   TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [7]
RP   SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Kidney;
RX   MEDLINE=89149813; PubMed=2493250;
RA   Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
RT   "Structure and expression of the alternatively-spliced forms of mRNA
RT   for the mouse homolog of Alzheimer's disease amyloid beta protein
RT   precursor.";
RL   Biochem. Biophys. Res. Commun. 158:906-912(1989).
RN   [8]
RP   SEQUENCE OF 289-364 FROM N.A.
RC   STRAIN=CD-1; TISSUE=Placenta;
RX   MEDLINE=89345111; PubMed=2569710;
RA   Fukuchi K., Martin G.M., Deeb S.S.;
RT   "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT   precursor of Mus domesticus.";
RL   Nucleic Acids Res. 17:5396-5396(1989).
RN   [9]
RP   SEQUENCE OF 656-737 FROM N.A.
RC   STRAIN=129/Sv;
RA   Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
RA   Loring J.F., Goate A.M.;
RT   "Introduction of six mutations into the mouse genome using 'Hit and
RT   Run' gene-targeting: introduction of familial Alzheimer's disease
RT   mutations into the mouse amyloid precursor protein gene and
RT   humanization of the A-beta fragment.";
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN   [10]
RP   TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
RX   MEDLINE=93287808; PubMed=8510506;
RA   Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
RT   "Regional distribution of the alternatively spliced isoforms of beta
RT   APP RNA transcript in the brain of normal, heterozygous and
RT   homozygous weaver mutant mice as revealed by in situ hybridization
RT   histochemistry.";
RL   Brain Res. Mol. Brain Res. 17:340-346(1993).
RN   [11]
RP   INTERACTION WITH KNS2.
RX   MEDLINE=21010507; PubMed=11144355;
RA   Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
RT   "Axonal transport of amyloid precursor protein is mediated by direct
RT   binding to the kinesin light chain subunit of kinesin-I.";
RL   Neuron 28:449-459(2000).
RN   [12]
RP   C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
RP   THR-743; TYR-757; ASN-759 AND TYR-762.
RX   MEDLINE=21408156; PubMed=11517249;
RA   Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA   Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
RA   Kyriakis J.M., Nishimoto I.;
RT   "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
RT   scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL   J. Neurosci. 21:6597-6607(2001).
RN   [13]
RP   INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
RX   MEDLINE=22028091; PubMed=11912189;
RA   Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
RT   "Interaction of Alzheimer's beta-amyloid precursor family proteins
RT   with scaffold proteins of the JNK signaling cascade.";
RL   J. Biol. Chem. 277:20070-20078(2002).
RN   [14]
RP   INTERACTION OF CTF PEPTIDES WITH NUMB.
RX   MEDLINE=22008109; PubMed=12011466;
RA   Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
RA   Meucci O., McGlade J.C., Rakic P., D'Adamio L.;
RT   "The gamma-secretase-generated intracellular domain of beta-amyloid
RT   precursor protein binds Numb and inhibits Notch signaling.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
RN   [15]
RP   GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.
RX   MEDLINE=21437805; PubMed=11553691;
RA   Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
RT   "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
RT   gamma-secretase is rapidly degraded but distributes partially in a
RT   nuclear fraction of neurones in culture.";
RL   J. Neurochem. 78:1168-1178(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions. Can promote transcription activation through binding
CC       to APBB1/Tip60 and inhibit Notch signaling through interaction
CC       with Numb. Couples to apoptosis-inducing pathways such as those
CC       mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity (By
CC       similarity). Acts as a kinesin I membrane receptor, mediating the
CC       axonal transport of beta-secretase and presenilin 1. May be
CC       involved in copper homeostasis/oxidative stress through copper ion
CC       reduction. Can regulate neurite outgrowth through binding to
CC       components of the extracellular matrix such as heparin and
CC       collagen I and IV (By similarity). The splice isoforms that
CC       contain the BPTI domain possess protease inhibitor activity (By
CC       similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC       only weakly transient metals and have little reducing activity due
CC       to substitutions of transient metal chelating residues. Beta-APP42
CC       may activate mononuclear phagocytes in the brain and elicit
CC       inflammatory responses. Promotes both tau aggregation and TPK II-
CC       mediated phosphorylation (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis.
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
CC       its serine phosphorylation. Also interacts with GPCR-like protein
CC       BPP, FPRL1, APPBP1, IB1, KNS2 (via its TPR domains), APPBP2 (via
CC       BaSS) and DDB1 (By similarity). In vitro, it binds MAPT via the
CC       MT-binding domains (By similarity). Associates with microtubules
CC       in the presence of ATP and in a kinesin-dependent manner (By
CC       similarity). Interacts, through a C-terminal domain, with GNAO1
CC       (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
CC       neurons (By similarity). Beta-amyloid associates with HADH2 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete

  Query Match             36.2%;  Score 64;  DB 1;  Length 770;
  Best Local Similarity   73.3%;  Pred. No. 0.3;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||| |||| :|| |:
Db        672 DAEFGHDSGFEVRHQ 686


RESULT 13
A4_RAT
ID   A4_RAT          STANDARD;      PRT;   770 AA.
AC   P08592;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble
DE   APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
DE   amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
DE   C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
DE   fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
```

DE Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact.";
RL EMBO J. 7:1365-1370(1988).
RN [2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
RN [3]
RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
RX MEDLINE=21443797; PubMed=11483588;
RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT family resembling gamma-secretase-like cleavage of Notch.";
RL J. Biol. Chem. 276:35235-35238(2001).
RN [4]
RP ALTERNATIVE SPLICING.
RX MEDLINE=96187032; PubMed=8624099;
RA Sandbrink R., Masters C.L., Beyreuther K.;
RT "APP gene family. Alternative splicing generates functionally related
RT isoforms.";
RL Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN [5]
RP TISSUE SPECIFICITY OF APPICAN.
RX MEDLINE=95263526; PubMed=7744833;
RA Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,
RA Mytilineou C., Margolis R.U., Robakis N.K.;
RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT brain and is produced by astrocytes but not by neurons in primary
RT neural cultures.";
RL J. Biol. Chem. 270:11839-11844(1995).
RN [6]
RP TISSUE SPECIFICITY OF ISOFORMS.
RX MEDLINE=97150061; PubMed=8996834;
RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
RT "Expression of the APP gene family in brain cells, brain development
RT and aging.";
RL Gerontology 43:119-131(1997).
RN [7]
RP INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
RP TYR-762.
RX MEDLINE=99127916; PubMed=9930726;
RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
RA Suzuki T., Nairn A.C., Greengard P.;
RT "A 127-kDa protein (UV-DDB) binds to the cytoplasmic domain of the
RT Alzheimer's amyloid precursor protein.";
RL J. Neurochem. 72:549-556(1999).
RN [8]
RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.
RX MEDLINE=99162676; PubMed=10024358;
RA Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouillot C.,
RA Valenza C., Prochiantz A., Allinquant B.;
RT "The amyloid precursor protein interacts with Go heterotrimeric
RT protein within a cell compartment specialized in signal
RT transduction.";
RL J. Neurosci. 19:1717-1727(1999).
RN [9]
RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
RX MEDLINE=95256193; PubMed=7737970;
RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
RT "The chondroitin sulfate attachment site of appican is formed by
RT splicing out exon 15 of the amyloid precursor gene.";
RL J. Biol. Chem. 270:10388-10391(1995).
RN [10]
RP BETA-AMYLOID METAL-BINDING.
RX MEDLINE=99316162; PubMed=10386999;
RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
RA Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
RA Bush A.I.;
RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
RT peroxide through metal ion reduction.";
RL Biochemistry 38:7609-7616(1999).
RN [11]
RP BETA-AMYLOID ZINC BINDING.
RX MEDLINE=99343552; PubMed=10413512;
RA Liu S.T., Howlett G., Barrow C.J.;
RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
RT of the A beta peptide of Alzheimer's disease.";
RL Biochemistry 38:9373-9378(1999).
RN [12]
RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
RP GLY-704.
RX MEDLINE=21956095; PubMed=11959460;
RA Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;
RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
RT peptide 1-42-associated oxidative stress and neurotoxicity.";
RL Biochim. Biophys. Acta 1586:190-198(2001).
RN [13]
RP PHOSPHORYLATION.
RX MEDLINE=97239592; PubMed=9085254;
RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
RA Greengard P., Suzuki T.;
RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
RT phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
RT cultured cells.";
RL Mol. Med. 3:111-123(1997).
RN [14]
RP PHOSPHORYLATION ON SER-730.
RX MEDLINE=99262094; PubMed=10329382;
RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
RA Greengard P., Nairn A.C., Suzuki T.;
RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
RT precursor protein at Ser655 by a novel protein kinase.";
RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
RN [15]
RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
RP THR-743.
RX MEDLINE=99274744; PubMed=10341243;
RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
RA Kirino Y., Greengard P., Suzuki T.;
RT "Role of phosphorylation of Alzheimer's amyloid precursor protein
RT during neuronal differentiation.";
RL J. Neurosci. 19:4421-4427(1999).
RN [16]
RP PHOSPHORYLATION ON THR-743.
RX MEDLINE=20396183; PubMed=10936190;
RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
RT protein by cyclin-dependent kinase 5.";
RL J. Neurochem. 75:1085-1091(2000).
RN [17]
RP CARBOHYDRATE STRUCTURE OF APPICAN.
RX MEDLINE=21463085; PubMed=11479316;
RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
RA Sugahara K., Robakis N.K.;
RT "Appican, the proteoglycan form of the amyloid precursor protein,
RT contains chondroitin sulfate E in the repeating disaccharide region
RT and 4-O-sulfated galactose in the linkage region.";
RL J. Biol. Chem. 276:37155-37160(2001).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to

```
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP. Inhibits
CC       G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
CC       mediating the axonal transport of beta-secretase and presenilin 1
CC       (By similarity). May be involved in copper homeostasis/oxidative
CC       stress through copper ion reduction. Can regulate neurite
CC       outgrowth through binding to components of the extracellular
CC       matrix such as heparin and collagen I and IV (By similarity). The
CC       splice isoforms that contain the BPTI domain possess protease
CC       inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC       only weakly transient metals and have little reducing activity due
CC       to substitutions of transient metal chelating residues. Beta-APP42
CC       may activate mononuclear phagocytes in the brain and elicit
CC       inflammatory responses. Promotes both tau aggregation and TPK II-
CC       mediated phosphorylation (By similarity).
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain.
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) (By similarity) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity). Interacts,
CC       through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
CC       CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
CC       associates with HADH2 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the

  Query Match             36.2%;  Score 64;  DB 1;  Length 770;
  Best Local Similarity   73.3%;  Pred. No. 0.3;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||| ||||:|| |:
Db        672 DAEFGHDSGFEVRHQ 686


RESULT 14
VGLF_RINDB
ID   VGLF_RINDB     STANDARD;      PRT;   546 AA.
AC   P41360;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Rinderpest virus (strain RBT1) (RDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=39007;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95088609; PubMed=7996154;
RA   Evans S.A., Baron M.D., Chamberlain R.W., Goatley L., Barrett T.;
RT   "Nucleotide sequence comparisons of the fusion protein gene from
RT   virulent and attenuated strains of rinderpest virus.";
RL   J. Gen. Virol. 75:3611-3617(1994).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z31656; CAA83482.1; -.
DR   PIR; S47300; S47300.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    546       FUSION GLYCOPROTEIN F0.
FT   CHAIN       20    108       F2 PROTEIN.
FT   CHAIN      109    546       F1 PROTEIN.
FT   DOMAIN     104    108       ARG/LYS-RICH (BASIC).
FT   TRANSMEM   109    133       POTENTIAL.
FT   TRANSMEM   484    513       POTENTIAL.
FT   DOMAIN     514    517       ARG/LYS-RICH (BASIC).
FT   DISULFID    64    191       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD    25     25       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    57     57       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    63     63       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   518    518       O-LINKED (POTENTIAL).
SQ   SEQUENCE   546 AA;  58418 MW;  38B539B89344F401 CRC64;

  Query Match             34.5%;  Score 61;  DB 1;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 0.56;
  Matches   11;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         17 SITEIKGVIVHRIETILF 34
              |::||||||||:| : :
Db        283 SLSEIKGVIVHRLEGVSY 300


RESULT 15
VGLF_RINDR
ID   VGLF_RINDR     STANDARD;      PRT;   546 AA.
AC   P41356;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Rinderpest virus (strain RBOK) (RDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=36409;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95088609; PubMed=7996154;
RA   Evans S.A., Baron M.D., Chamberlain R.W., Goatley L., Barrett T.;
RT   "Nucleotide sequence comparisons of the fusion protein gene from
RT   virulent and attenuated strains of rinderpest virus.";
RL   J. Gen. Virol. 75:3611-3617(1994).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
```

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CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Z30700; CAA83186.1; -.
DR   EMBL; Z30697; CAA83181.1; -.
DR   PIR; S47305; S47305.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    546       FUSION GLYCOPROTEIN F0.
FT   CHAIN        20    108       F2 PROTEIN.
FT   CHAIN       109    546       F1 PROTEIN.
FT   DOMAIN      104    108       ARG/LYS-RICH (BASIC).
FT   TRANSMEM    109    133       POTENTIAL.
FT   TRANSMEM    484    513       POTENTIAL.
FT   DOMAIN      514    517       ARG/LYS-RICH (BASIC).
FT   DISULFID     64    191       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD     25     25       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     57     57       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     63     63       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    518    518       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   546 AA;  58705 MW;  ED3DF8AFFDBECB95 CRC64;

  Query Match             33.9%;  Score 60;  DB 1;  Length 546;
  Best Local Similarity   55.6%;  Pred. No. 0.77;
  Matches   10;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         17 SITEIKGVIVHRIETILF 34
              |::||||||:||:| : :
Db        283 SLSEIKGVIIHRLEGVSY 300


Search completed: June 18, 2004, 19:59:38
Job time : 7.67485 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:15 ; Search time 32.9571 Seconds
(without alignments)
325.503 Million cell updates/sec

Title: US-09-865-294A-73
Perfect score: 177
Sequence: 1 DAEFRHDSGYEVHHKISITEIKGVIVHRIETILF 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	85	48.0	82	4	Q16014	Q16014 homo sapien
2	83	46.9	19	4	Q9UCC8	Q9ucc8 homo sapien
3	83	46.9	28	4	Q9UCD1	Q9ucd1 homo sapien
4	83	46.9	30	4	Q9UCA9	Q9uca9 homo sapien
5	83	46.9	33	4	Q9UC33	Q9uc33 homo sapien
6	83	46.9	82	4	Q16020	Q16020 homo sapien
7	83	46.9	82	4	Q16019	Q16019 homo sapien
8	83	46.9	113	13	Q8JH58	Q8jh58 chelydra se
9	83	46.9	534	13	O93296	O93296 gallus gall
10	83	46.9	569	13	Q9PVL1	Q9pvl1 gallus gall
11	83	46.9	695	13	Q9DGJ8	Q9dgj8 gallus gall
12	83	46.9	751	13	Q9DGJ7	Q9dgj7 gallus gall
13	78	44.1	35	4	Q8WZ99	Q8wz99 homo sapien
14	68	38.4	693	13	Q98SG0	Q98sg0 xenopus lae
15	68	38.4	695	13	Q98SF9	Q98sf9 xenopus lae
16	68	38.4	695	13	Q7ZXQ0	Q7zxq0 xenopus lae
17	68	38.4	747	13	Q91963	Q91963 xenopus. ap
18	64	36.2	79	11	O35463	O35463 cricetulus
19	64	36.2	218	11	Q8BPV5	Q8bpv5 mus musculu
20	64	36.2	384	11	Q8BPC7	Q8bpc7 mus musculu
21	63	35.6	699	13	O57394	O57394 narke japon
22	61	34.5	546	12	Q91HA5	Q91ha5 rinderpest
23	60	33.9	546	12	Q84926	Q84926 peste-des-p
24	59	33.3	528	12	Q9YJW9	Q9yjw9 canine dist
25	59	33.3	530	12	Q8QV06	Q8qv06 canine dist
26	59	33.3	552	12	Q66147	Q66147 cetacean mo
27	59	33.3	662	12	Q9DXZ2	Q9dxz2 canine dist
28	59	33.3	662	12	Q91KN3	Q91kn3 canine dist
29	59	33.3	662	12	Q9YKL7	Q9ykl7 canine dist
30	59	33.3	662	12	O89327	O89327 canine dist
31	58	32.8	319	10	Q9LTT3	Q9ltt3 arabidopsis
32	58	32.8	534	12	Q04243	Q04243 measles vir
33	58	32.8	537	12	Q04242	Q04242 measles vir
34	58	32.8	545	12	Q9PXA4	Q9pxa4 measles vir
35	58	32.8	550	12	P90331	P90331 measles vir
36	58	32.8	550	12	Q9QEX0	Q9qex0 measles vir
37	58	32.8	550	12	Q9QEW9	Q9qew9 measles vir
38	58	32.8	550	12	P90330	P90330 measles vir
39	58	32.8	550	12	Q9QEW7	Q9qew7 measles vir
40	58	32.8	550	12	Q9WMK4	Q9wmk4 measles vir
41	58	32.8	550	12	Q89495	Q89495 measles vir
42	58	32.8	550	12	Q8V049	Q8v049 measles vir
43	58	32.8	550	12	Q9YJ94	Q9yj94 measles vir
44	58	32.8	550	12	Q9QEX1	Q9qex1 measles vir
45	58	32.8	550	12	Q9QEW8	Q9qew8 measles vir

ALIGNMENTS

RESULT 1
Q16014
ID Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzcwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26263.2; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 48.0%; Score 85; DB 4; Length 82;
Best Local Similarity 43.5%; Pred. No. 0.00013;
Matches 20; Conservative 5; Mismatches 9; Indels 12; Gaps 2;

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Qy          1 DAEFRHDSGYEVHHK------ISITEIKGVIVHR------IETILF 34
              |||||||||||||:        :   || |:        | |::|
Db         18 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIF 63
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RESULT 2
Q9UCC8

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ID   Q9UCC8      PRELIMINARY;      PRT;    19 AA.
AC   Q9UCC8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid-(1-42) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94068497; PubMed=8248178;
RA   Roher A.E., Lowenson J.D., Clarke S., Woods A.S., Cotter R.J.,
RA   Gowing E., Ball M.J.;
RT   "beta-Amyloid-(1-42) is a major component of cerebrovascular amyloid
RT   deposits: implications for the pathology of Alzheimer disease.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:10836-10840(1993).
DR   HSSP; P05067; 1AMB.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   19 AA;  2315 MW;  05B02B3F6DDECE3E CRC64;

  Query Match             46.9%;  Score 83;  DB 4;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 5.1e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||:
Db          1 DAEFRHDSGYEVHHQ 15


RESULT 3
Q9UCD1
ID   Q9UCD1      PRELIMINARY;      PRT;    28 AA.
AC   Q9UCD1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94045685; PubMed=8229004;
RA   Vigo-Pelfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;
RT   "Characterization of beta-amyloid peptide from human cerebrospinal
RT   fluid.";
RL   J. Neurochem. 61:1965-1968(1993).
DR   HSSP; P05067; 1AMB.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   28 AA;  3244 MW;  DE7BD081160AFC81 CRC64;

  Query Match             46.9%;  Score 83;  DB 4;  Length 28;
  Best Local Similarity   93.3%;  Pred. No. 7.8e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||:
Db          1 DAEFRHDSGYEVHHQ 15


RESULT 4
Q9UCA9
ID   Q9UCA9      PRELIMINARY;      PRT;    30 AA.
AC   Q9UCA9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94153015; PubMed=8109908;
RA   Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;
RT   "The amino acid sequence of neuritic plaque amyloid from a familial
RT   Alzheimer's disease patient.";
RL   Ann. Neurol. 35:245-246(1994).
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   30 AA;  3391 MW;  FF4167ABD081160A CRC64;

  Query Match             46.9%;  Score 83;  DB 4;  Length 30;
  Best Local Similarity   93.3%;  Pred. No. 8.4e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||:
Db          1 DAEFRHDSGYEVHHQ 15


RESULT 5
Q9UC33
ID   Q9UC33      PRELIMINARY;      PRT;    33 AA.
AC   Q9UC33;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=93024877; PubMed=1406936;
RA   Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA   Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT   "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT   biological fluids.";
RL   Nature 359:325-327(1992).
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   33 AA;  3674 MW;  B1DEFE2F4167ABD0 CRC64;

  Query Match             46.9%;  Score 83;  DB 4;  Length 33;
  Best Local Similarity   93.3%;  Pred. No. 9.3e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||:
Db          1 DAEFRHDSGYEVHHQ 15


RESULT 6
Q16020
ID   Q16020      PRELIMINARY;      PRT;    82 AA.
AC   Q16020;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
GN   BETA APP.
OS   Homo sapiens (Human).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S61383; AAB26265.2; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8882 MW;  F534AA5AE5D9230A CRC64;

  Query Match             46.9%;  Score 83;  DB 4;  Length 82;
  Best Local Similarity   93.3%;  Pred. No. 0.00025;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||||:
Db         18 DAEFRHDSGYEVHHQ 32


RESULT 7
Q16019
ID   Q16019      PRELIMINARY;      PRT;    82 AA.
AC   Q16019;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
GN   BETA APP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S61380; AAB26264.2; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8938 MW;  F534AA50E579230A CRC64;

  Query Match             46.9%;  Score 83;  DB 4;  Length 82;
  Best Local Similarity   93.3%;  Pred. No. 0.00025;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||||:
Db         18 DAEFRHDSGYEVHHQ 32


RESULT 8
Q8JH58
ID   Q8JH58      PRELIMINARY;      PRT;   113 AA.
AC   Q8JH58;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid beta protein (Fragment).
OS   Chelydra serpentina serpentina (common snapping turtle).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX   NCBI_TaxID=134619;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21876906; PubMed=11882478;
RA   Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT   "Octylphenol (OP) alters the expression of members of the amyloid
RT   protein family in the hypothalamus of the snapping turtle, Chelydra
RT   serpentina serpentina.";
RL   Environ. Health Perspect. 110:269-275(2002).
DR   EMBL; AF541917; AAN04908.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   113 AA;  12750 MW;  72515C930496E053 CRC64;

  Query Match             46.9%;  Score 83;  DB 13;  Length 113;
  Best Local Similarity   93.3%;  Pred. No. 0.00036;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||||:
Db         15 DAEFRHDSGYEVHHQ 29


RESULT 9
O93296
ID   O93296      PRELIMINARY;      PRT;   534 AA.
AC   O93296;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid protein (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98337885; PubMed=9671674;
RA   Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA   Milligan C.E.;
RT   "Increased production of amyloid precursor protein provides a
RT   substrate for caspase-3 in dying motoneurons.";
RL   J. Neurosci. 18:5869-5880(1998).
DR   EMBL; AF042098; AAC25052.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   534 AA;  60597 MW;  FB53ECC2B66D4C92 CRC64;

  Query Match             46.9%;  Score 83;  DB 13;  Length 534;
  Best Local Similarity   93.3%;  Pred. No. 0.002;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||||:
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Db        436 DAEFRHDSGYEVHHQ 450


RESULT 10
Q9PVL1
ID   Q9PVL1      PRELIMINARY;      PRT;   569 AA.
AC   Q9PVL1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid protein (Fragment).
GN   APP.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT   "What the evolution of the amyloid protein precursor supergene family
RT   tells us about its function.";
RL   Neurochem. Int. 0:0-0(2000).
DR   EMBL; AF030341; AAF12698.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   569 AA;  64753 MW;  0AB8BB851863A19D CRC64;

  Query Match             46.9%;  Score 83;  DB 13;  Length 569;
  Best Local Similarity   93.3%;  Pred. No. 0.0022;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||||:
Db        472 DAEFRHDSGYEVHHQ 486


RESULT 11
Q9DGJ8
ID   Q9DGJ8      PRELIMINARY;      PRT;   695 AA.
AC   Q9DGJ8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid precursor protein 695 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289218; AAG00593.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   695 AA;  78565 MW;  F201ED02AEC86D95 CRC64;

  Query Match             46.9%;  Score 83;  DB 13;  Length 695;
  Best Local Similarity   93.3%;  Pred. No. 0.0027;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||||:
Db        597 DAEFRHDSGYEVHHQ 611


RESULT 12
Q9DGJ7
ID   Q9DGJ7      PRELIMINARY;      PRT;   751 AA.
AC   Q9DGJ7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid precursor protein 751 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289219; AAG00594.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   751 AA;  84705 MW;  B78E9413A8033D84 CRC64;

  Query Match             46.9%;  Score 83;  DB 13;  Length 751;
  Best Local Similarity   93.3%;  Pred. No. 0.0029;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||||||||||:
Db        653 DAEFRHDSGYEVHHQ 667


RESULT 13
Q8WZ99
ID   Q8WZ99      PRELIMINARY;      PRT;    35 AA.
AC   Q8WZ99;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
```

```
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Amyloid protein (Fragment).
GN   APP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wakutani Y., Ninomiya H., Iwata H., Tanaka S., Urakami K., Adachi Y.,
RA   Wada-Isoe K., Yamagata K., Ohono K., Tsubuki S., Saido T.,
RA   Hashimoto T., Iwatsubo T., Nakashima K.;
RT   "Novel missense mutation (D678N) of amyloid precursor protein gene in
RT   a Japanese pedigree of familial Alzheimer's disease.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB066441; BAB71958.1; -.
FT   NON_TER       1      1
FT   NON_TER      35     35
SQ   SEQUENCE   35 AA;  4084 MW;  49D7D17289743B71 CRC64;

  Query Match             44.1%;  Score 78;  DB 4;  Length 35;
  Best Local Similarity   86.7%;  Pred. No. 0.00053;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |||||||:|||||||:
Db         17 DAEFRHNSGYEVHHQ 31


RESULT 14
Q98SG0
ID   Q98SG0      PRELIMINARY;      PRT;   693 AA.
AC   Q98SG0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid precursor protein A.
GN   APP.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van den Hurk W.H.;
RL   Thesis (2001), Department of Biological Sciences,
RL   University of Nijmegen, Nijmegen, Netherlands.
DR   EMBL; AJ298150; CAC37193.1; -.
DR   HSSP; P05067; 1HZ3.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal.
FT   SIGNAL        1     18       POTENTIAL.
SQ   SEQUENCE   693 AA;  78568 MW;  CAF1DF655C1AB653 CRC64;

  Query Match             38.4%;  Score 68;  DB 13;  Length 693;
  Best Local Similarity   66.7%;  Pred. No. 0.4;
  Matches   10;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |:|:|||: |||||:
Db        595 DSEYRHDTAYEVHHQ 609


RESULT 15
Q98SF9
ID   Q98SF9      PRELIMINARY;      PRT;   695 AA.
AC   Q98SF9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid precursor protein B.
GN   APP.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van den Hurk W.H.;
RL   Thesis (2001), Department of Biological Sciences,
RL   University of Nijmegen, Nijmegen, Netherlands.
DR   EMBL; AJ298151; CAC37194.1; -.
DR   HSSP; P05067; 1HZ3.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal.
FT   SIGNAL        1     18       POTENTIAL.
SQ   SEQUENCE   695 AA;  78803 MW;  DC14EB02AFB0204A CRC64;

  Query Match             38.4%;  Score 68;  DB 13;  Length 695;
  Best Local Similarity   66.7%;  Pred. No. 0.41;
  Matches   10;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHK 15
              |:|:|||: |||||:
Db        597 DSEYRHDAAYEVHHQ 611


Search completed: June 18, 2004, 20:02:29
Job time : 32.9571 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:20 ; Search time 69.2025 Seconds
(without alignments)
195.980 Million cell updates/sec

Title: US-09-865-294A-74
Perfect score: 247
Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....KISITEIKGVIVHRIETILP 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	247	100.0	48	6	AAE35680	Aae35680 Human Abe
2	163	66.0	100	5	AAE14375	Aae14375 Amyloid p
3	163	66.0	108	5	AAE14383	Aae14383 Gamma-sec
4	163	66.0	112	2	AAR93556	Aar93556 Familial
5	163	66.0	695	2	AAW19484	Aaw19484 APP695 mu
6	163	66.0	695	2	AAW19498	Aaw19498 APP695 mu
7	163	66.0	695	3	AAY88436	Aay88436 Human APP
8	163	66.0	695	4	AAU07207	Aau07207 Human bet
9	163	66.0	695	4	AAE10634	Aae10634 Human amy
10	163	66.0	695	4	AAE06864	Aae06864 Human amy
11	163	66.0	695	4	AAE02586	Aae02586 Human amy
12	163	66.0	695	4	AAU06608	Aau06608 Human Amy
13	163	66.0	695	5	ABB78595	Abb78595 Human APP
14	163	66.0	697	3	AAY88430	Aay88430 Human APP
15	163	66.0	697	4	AAU07210	Aau07210 Human bet
16	163	66.0	697	4	AAE10637	Aae10637 Human amy
17	163	66.0	697	4	AAE06867	Aae06867 Human amy
18	163	66.0	697	4	AAE02589	Aae02589 Human amy
19	163	66.0	697	4	AAU06611	Aau06611 Human Amy
20	163	66.0	697	5	ABB78598	Abb78598 Human APP
21	163	66.0	751	2	AAW19486	Aaw19486 APP751 mu
22	163	66.0	751	2	AAW19499	Aaw19499 APP751 mu
23	163	66.0	770	2	AAW19485	Aaw19485 APP770 mu
24	163	66.0	770	2	AAW19500	Aaw19500 APP770 mu
25	163	66.0	770	4	AAE06913	Aae06913 Human amy
26	161.5	65.4	42	2	AAR65288	Aar65288 Beta amyl
27	160	64.8	34	6	AAB35679	Aae35679 Human Abe
28	158.5	64.2	42	2	AAR65287	Aar65287 Beta amyl
29	158	64.0	118	2	AAW50030	Aaw50030 APP C-ter
30	157	63.6	47	2	AAW81475	Aaw81475 Synthetic
31	157	63.6	48	4	AAB37523	Aab37523 Amyloid p
32	157	63.6	52	2	AAR64166	Aar64166 Variant b
33	157	63.6	52	2	AAW81476	Aaw81476 Synthetic
34	157	63.6	52	6	ABU08712	Abu08712 Amlyoid b
35	157	63.6	52	6	ABP97924	Abp97924 Amino aci
36	157	63.6	52	6	ADA90299	Ada90299 Abeta ami
37	157	63.6	53	2	AAR55695	Aar55695 Sequence
38	157	63.6	53	6	ABU08708	Abu08708 Amlyoid b
39	157	63.6	53	7	ADB61450	Adb61450 Amyloid b
40	157	63.6	54	3	AAB32126	Aab32126 Amyloid-b
41	157	63.6	55	4	AAB11482	Aab11482 Human APP
42	157	63.6	59	2	AAW05375	Aaw05375 Amyloid p
43	157	63.6	59	2	AAW70863	Aaw70863 Beta-amyl
44	157	63.6	59	4	AAB84425	Aab84425 Partial s
45	157	63.6	60	3	AAY69701	Aay69701 Beta-amyl

ALIGNMENTS

RESULT 1
AAE35680
ID AAE35680 standard; peptide; 48 AA.
XX
AC AAE35680;
XX
DT 23-OCT-2003 (revised)
DT 17-JUN-2003 (first entry)
XX
DE Human Abeta peptide-measles virus Th epitope fusion peptide immunogen #4.
XX
KW Immunogen; helper T cell; Th epitope; amyloid beta; Alzheimer's disease;
KW Abeta; AD; brain tissue plaque; immunoneutralisation; neuroprotective;
KW vaccine; nootropic; human; hepatitis B virus; HBV; fusion peptide.
XX
OS Homo sapiens.
OS Measles virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1. .28
FT /note= "Human beta amyloid peptide"
FT Region 32. .48
FT /note= "Measles virus T helper cell epitope"
XX
PN WO200296350-A2.
XX
PD 05-DEC-2002.
XX
PF 02-APR-2002; 2002WO-US010293.
XX
PR 25-MAY-2001; 2001US-00865294.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2003-201258/19.
XX
PT Novel peptide immunogen comprising a helper T cell epitope, an N-terminal
PT fragment of amyloid beta peptide linked to the epitope, and optionally a
PT spacer, useful for preventing or treating Alzheimer's disease.
XX
PS Claim 9; Page 39; 77pp; English.
XX
CC The present invention relates to a novel peptide immunogen comprising a
CC helper T cell (Th) epitope, an N-terminal fragment of amyloid beta
CC (Abeta) peptide (residues 1-42) linked to the epitope and optionally a

CC spacer consisting of at least an amino acid to separate the immunogenic
CC domains. Sequences of the invention are useful for preventing or treating
CC Alzheimer's disease (AD) in a mammal, to produce antibodies to Abeta
CC peptide that is cross-reactive to soluble Abeta peptides and brain tissue
CC plaques formed from it. They are useful for eliciting a site-directed
CC mutagenesis against the main functional/regulatory site of the Abeta
CC peptide and for generating antibodies, which are highly cross-reactive to
CC the soluble Abeta peptide and the amyloid plaques formed in the brain of
CC Alzheimer's disease patients. The sequences are useful for induction of
CC accelerated clearance of amyloid plaques and immunoneutralisation of the
CC soluble Abeta derived toxins in the brain to prevent and treat
CC Alzheimer's disease. They are also useful as vaccines. The present
CC sequence is human Abeta peptide-measles virus T helper cell epitope
CC fusion peptide immunogen used in the exemplification of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 48 AA;

Query Match 100.0%; Score 247; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 5e-27;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48

RESULT 2
AAE14375
ID AAE14375 standard; peptide; 100 AA.
XX
AC AAE14375;
XX
DT 12-MAR-2002 (first entry)
XX
DE Amyloid precursor protein beta-CTF domain #5.
XX
KW Gamma-secretase substrate; beta-CTF domain; amyloid precursor protein;
KW APP; beta-secretase; Alzheimer's disease.
XX
OS Unidentified.
XX
PN WO200183811-A1.
XX
PD 08-NOV-2001.
XX
PF 25-APR-2001; 2001WO-US013332.
XX
PR 01-MAY-2000; 2000US-0201053P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Li Y, Xu M, Huang Q, Gardell S;
XX
DR WPI; 2002-066536/09.
XX
PT Novel gamma secretase substrate for assaying gamma secretase activity and
PT identifying compounds that regulate gamma secretase activity, e.g.
PT inhibitors of gamma secretase useful for treating Alzheimer's disease.
XX
PS Claim 3; Page 6; 36pp; English.
XX
CC The invention relates to gamma-secretase substrates containing a
CC hydrophilic polypeptide moiety covalently joined to the carboxyl terminus
CC of a beta-CTF domain. A beta-CTF domain is a polypeptide that can be
CC cleaved by gamma-secretase, and that approximates the C-terminal fragment
CC (amino acids 596-695) of amyloid precursor protein (APP) produced after
CC cleavage of APP by beta-secretase. The hydrophilic polypeptide moiety
CC increases the solubility of the substrate in a zwitterionic detergent.
CC The gamma-secretase substrate is used in in vitro assays employing
CC zwitterionic detergent for measuring gamma-secretase activity. The assay
CC methods are useful for purifying and characterising the enzyme, to screen
CC for compounds that modulate gamma-secretase activity, and to test the
CC ability of a particular compound that affect gamma-secretase activity.
CC The compounds that modulate gamma-secretase activity include gamma-
CC secretase inhibitors which are useful in the treatment of Alzheimer's
CC disease, and in the characterisation of the biological importance of
CC gamma-secretase. The present sequence is a beta-CTF domain used in the
CC invention
XX
SQ Sequence 100 AA;

Query Match 66.0%; Score 163; DB 5; Length 100;
Best Local Similarity 70.8%; Pred. No. 7.7e-15;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
|||||||||||||||||||||||||||| | : | :| | |::|
Db 2 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 47

RESULT 3
AAE14383
ID AAE14383 standard; protein; 108 AA.
XX
AC AAE14383;
XX
DT 12-MAR-2002 (first entry)
XX
DE Gamma-secretase substrate #5.
XX
KW Gamma-secretase substrate; beta-CTF domain; amyloid precursor protein;
KW APP; beta-secretase; Alzheimer's disease; fusion protein.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Region 1. .100
FT /label= Beta-CTF_domain
FT Region 101. .108
FT /note= "Hydrophilic moiety"
XX
PN WO200183811-A1.
XX
PD 08-NOV-2001.
XX
PF 25-APR-2001; 2001WO-US013332.
XX
PR 01-MAY-2000; 2000US-0201053P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Li Y, Xu M, Huang Q, Gardell S;
XX
DR WPI; 2002-066536/09.
XX
PT Novel gamma secretase substrate for assaying gamma secretase activity and
PT identifying compounds that regulate gamma secretase activity, e.g.
PT inhibitors of gamma secretase useful for treating Alzheimer's disease.
XX
PS Claim 8; Page 8; 36pp; English.
XX
CC The invention relates to gamma-secretase substrates containing a
CC hydrophilic polypeptide moiety covalently joined to the carboxyl terminus
CC of a beta-CTF domain. A beta-CTF domain is a polypeptide that can be
CC cleaved by gamma-secretase, and that approximates the C-terminal fragment
CC (amino acids 596-695) of amyloid precursor protein (APP) produced after
CC cleavage of APP by beta-secretase. The hydrophilic polypeptide moiety
CC increases the solubility of the substrate in a zwitterionic detergent.
CC The gamma-secretase substrate is used in in vitro assays employing
CC zwitterionic detergent for measuring gamma-secretase activity. The assay
CC methods are useful for purifying and characterising the enzyme, to screen
CC for compounds that modulate gamma-secretase activity, and to test the
CC ability of a particular compound that affect gamma-secretase activity.
CC The compounds that modulate gamma-secretase activity include gamma-
CC secretase inhibitors which are useful in the treatment of Alzheimer's

```
CC   disease, and in the characterisation of the biological importance of
CC   gamma-secretase. The present sequence is an example of gamma-secretase
CC   substrate of the invention. The substrate is a fusion protein containing
CC   APP beta-CTF domain and a hydrophilic moiety
XX
SQ   Sequence 108 AA;

  Query Match             66.0%;  Score 163;  DB 5;  Length 108;
  Best Local Similarity   70.8%;  Pred. No. 8.5e-15;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
              |||||||||||||||||||||||||||||   |  : | :|  | |::|
Db          2 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 47


RESULT 4
AAR93556
ID   AAR93556 standard; protein; 112 AA.
XX
AC   AAR93556;
XX
DT   10-OCT-1996  (first entry)
XX
DE   Familial Alzheimer's disease APP isoform 751 fragment.
XX
KW   APP; amyloid precursor protein; isoform 751; inherent; familial;
KW   Alzheimer's disease; mutation; diagnosis; transgenic model; study;
KW   cognitive; beta A4 domain; exon 17; senility.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          14. .56
FT                   /label= beta-A4_domain
FT   Misc-difference 59
FT                   /note= "corresponds to bases 175-177 in file AAT18082, a
FT                   TTC codon, this translation exception is the site of a
FT                   Val to Ile mutation in isoform 751, bases 175-177
FT                   probably should be ATC and not TTC"
XX
PN   WO9606927-A1.
XX
PD   07-MAR-1996.
XX
PF   28-AUG-1995;   95WO-US010920.
XX
PR   01-SEP-1994;   94US-00299872.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Singh G,  Chen HY,  Heavens RP,  Sirinathsinghji DJS,  Smith DW;
PI   Trumbauer ME,  Van Der Ploeg LHT,  Vongs A,  Zheng H;
XX
DR   WPI; 1996-160358/16.
DR   N-PSDB; AAT18082.
XX
PT   Transgenic animal expressing familial form of human amyloid precursor
PT   protein - used to evaluate compounds affecting Alzheimer's disease and
PT   other cognitive disorders.
XX
PS   Example 1; Fig 7; 32pp; English.
XX
CC   AAR93556 is a fragment of the amyloid precursor protein (APP) isoform 751
CC   from a patient diagnosed with familial Alzheimer's disease (FAD). The
CC   sequence given corresponds to amino acids 640-751 of FAD APP 751. A
CC   feature of FAD is a Val to Ile substitution at posn. 698 of the full APP
CC   (posn. 59 of this sequence). DNA encoding this sequence was used to
CC   construct expression vectors for the prodn. of transgenic animals (esp.
CC   mice) carrying the FAD APP 751 mutation. The transgenic animals are
CC   useful for the evaluation of test cpds. affecting Alzheimer's disease and
CC   other cognitive disorders and for identification of new targets in
CC   Alzheimer's disease since the progression of the disease can be followed
CC   gradually. N.B. the V-I mutation at posn. 59 is given in the
CC   specification as being encoded by a TTC codon (most probably this should
CC   be ATC)
XX
SQ   Sequence 112 AA;

  Query Match             66.0%;  Score 163;  DB 2;  Length 112;
  Best Local Similarity   70.8%;  Pred. No. 8.9e-15;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
              |||||||||||||||||||||||||||||   |  : | :|  | |::|
Db         14 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 59


RESULT 5
AAW19484
ID   AAW19484 standard; protein; 695 AA.
XX
AC   AAW19484;
XX
DT   08-SEP-1997  (first entry)
XX
DE   APP695 mutant A-beta-containing protein.
XX
KW   Alzheimer's disease; transgenic mammal; beta-amyloid precursor protein;
KW   APP.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 642
FT                   /note= "Wild-type Val is preferably substituted by Phe"
XX
PN   WO9640895-A1.
XX
PD   19-DEC-1996.
XX
PF   07-JUN-1996;   96WO-US009679.
XX
PR   07-JUN-1995;   95US-00486018.
PR   07-JUN-1995;   95US-00486538.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Mcconlogue LC,  Seubert PA;
XX
DR   WPI; 1997-052308/05.
XX
PT   Transgenic mammal comprising DNA encoding A-beta-contg. protein - useful
PT   as animal model to test potential Alzheimer's disease treatments.
XX
PS   Claim 11; Page; 116pp; English.
XX
CC   A novel non-human transgenic mammal has been produced which contains a
CC   nucleic acid construct for expression of A-beta- containing protein,
CC   stably incorporated into its genome. The construct comprises a promoter,
CC   for expression in a mammalian cell, operably linked to a region encoding
CC   the A-beta-containing protein, which includes amino acids 672-714 of
CC   human beta-amyloid precursor protein (APP), where the region is selected
CC   from DNA encoding the A-beta-containing protein consisting of all, or a
CC   contiguous portion of APP770, APP751 or APP695, or a mutant comprising a
CC   mutation in one or more of amino acids 669, 670, 671, 690, 692 and 717.
CC   The present sequence represents a mutant APP695 protein in which the
CC   codon encoding amino acid 717 is mutated from wild-type Val to Phe. The
CC   amino acid positions referred to in the specification are as they appear
CC   in APP770 (see AAW19482) i.e. position 717 represents position 642 in
CC   APP695, and 698 in APP751. The larger forms of APP (APP751, APP770)
CC   consist of APP695 plus one or two additional domains. The transgenic
CC   mammal is used as an animal model to test compounds for an effect on the
CC   expression or processing of an A-beta-containing protein, i.e. to test
CC   potential Alzheimer's disease treatments. N.B. The present sequence is
CC   shown in the specification, but has been derived from SEQ ID NO:2 which
```

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CC   is on pages 82-84
XX
SQ   Sequence 695 AA;

  Query Match             66.0%;  Score 163;  DB 2;  Length 695;
  Best Local Similarity   70.8%;  Pred. No. 9.5e-14;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
              |||||||||||||||||||||||||||||    |  : | :|  | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642


RESULT 6
AAW19498
ID   AAW19498 standard; protein; 695 AA.
XX
AC   AAW19498;
XX
DT   08-SEP-1997  (first entry)
XX
DE   APP695 mutant A-beta-containing protein.
XX
KW   Alzheimer's disease; transgenic mammal; beta-amyloid precursor protein;
KW   APP.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 642
FT                   /note= "Wild-type Val is preferably substituted by Phe"
XX
PN   WO9640896-A1.
XX
PD   19-DEC-1996.
XX
PF   07-JUN-1996;   96WO-US009857.
XX
PR   07-JUN-1995;   95US-00480653.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Games KD,  Schenk DB,  Mcconlogue LC,  Seubert PA,  Rydel RE;
XX
DR   WPI; 1997-052309/05.
XX
PT   Testing compounds for an effect on an Alzheimer's disease marker - uses
PT   non-human transgenic animals which can control expression of major forms
PT   of beta-amyloid precursor protein.
XX
PS   Claim 23; Page; 139pp; English.
XX
CC   A novel method has been produced for testing compounds for an effect on
CC   an Alzheimer's disease (AD) marker. The method involves: administering
CC   the compound to be tested to a non-human transgenic mammal, or mammalian
CC   cells derived from the transgenic mammal, where the transgenic mammal has
CC   a nucleic acid construct stably incorporated into the genome which
CC   comprises a promoter for expression of the construct in a mammalian cell
CC   operably linked to a region encoding an A-beta-containing protein. The
CC   region is selected from DNA encoding the A-beta-containing protein
CC   consisting of all, or a contiguous portion of APP770, APP751 or APP695,
CC   or a mutant comprising a mutation in one or more of amino acids 669, 670,
CC   671, 690, 692 and 717, which includes amino acids 672-714 of human beta-
CC   amyloid precursor protein (APP). The present sequence represents a mutant
CC   APP695 protein in which the codon encoding amino acid 717 is mutated (see
CC   features table). The amino acid positions referred to in the
CC   specification are as they appear in APP770 (see AAW19497) i.e. position
CC   717 represents position 642 in APP695, and 698 in APP751. The larger
CC   forms of APP (APP751, APP770) consist of APP695 plus one or two
CC   additional domains. The method also involves detecting or measuring the
CC   AD marker such that any difference between the marker in the transgenic
CC   animal, or mammalian cells derived from the transgenic mammal, to which
CC   the compound has not been administered, is observed, where an observed
CC   difference in the marker indicates that the compound has an effect on the
CC   marker. The transgenic animals, or cells are used to screen for compounds
CC   which alter the pathological course of AD as measured by their effect on
CC   the amount and/or histopathology of AD markers in animals as well as
CC   behavioural alterations. N.B. The present sequence is shown in the
CC   specification, but has been derived from SEQ ID NO:2 which is on pages
CC   103-105
XX
SQ   Sequence 695 AA;

  Query Match             66.0%;  Score 163;  DB 2;  Length 695;
  Best Local Similarity   70.8%;  Pred. No. 9.5e-14;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
              |||||||||||||||||||||||||||||    |  : | :|  | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642


RESULT 7
AAY88436
ID   AAY88436 standard; protein; 695 AA.
XX
AC   AAY88436;
XX
DT   03-AUG-2000  (first entry)
XX
DE   Human APP695-VF amino acid sequence.
XX
KW   Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW   Alzheimer's disease; beta secretase site; APP695-VF.
XX
OS   Homo sapiens.
XX
PN   WO200017369-A2.
XX
PD   30-MAR-2000.
XX
PF   23-SEP-1999;   99WO-US020881.
XX
PR   24-SEP-1998;   98US-0101594P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Gurney ME,  Bienkowski MJ,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2000-303209/26.
DR   N-PSDB; AAA15676.
XX
PT   New enzyme designated human aspartase useful in research into Alzheimer's
PT   Disease is capable of cleaving amyloid protein precursor at the beta
PT   secretase site to produce amyloid beta peptide.
XX
PS   Example 8; Page 131-135; 183pp; English.
XX
CC   This sequence represents a modified version of the human amyloid
CC   precursor protein 695 (APP695) amino acid sequence. The sequence is used
CC   in an example of the invention, showing the activity of Hu-asp2. The
CC   invention relates to a protease (e.g. Asp2) capable of cleaving the beta
CC   secretase site of amyloid precursor protein (APP). The protease contains
CC   a sequence encoding the amino acid sequence DTG and a sequence encoding
CC   DSG or DTG separated by 100-300 amino acids. When mutated the APP gene
CC   causes an autosomal dominant form of Alzheimer's disease. APP localises
CC   to the cell surface membrane and have a single C-terminal transmembrane
CC   domain. Proteolytic processing of APP produces the amyloid beta protein,
CC   which is possibly very important in Alzheimer's disease. The invention
CC   includes a nucleotide sequence encoding the protease, a vector containing
CC   the nucleotide sequence, and a cell line comprising the vector. Methods
CC   for screening for inhibitors of beta secretase activity are also given in
CC   the invention. The human aspartase protein and nucleotide sequences and
CC   the methods for identifying inhibitors of the protease, are useful in the
CC   treatment of and research in to Alzheimer's disease
XX
```

```
SQ   Sequence 695 AA;

  Query Match             66.0%;  Score 163;  DB 3;  Length 695;
  Best Local Similarity   70.8%;  Pred. No. 9.5e-14;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
              |||||||||||||||||||||||||||||||   |  : | :|  | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642


RESULT 8
AAU07207
ID   AAU07207 standard; protein; 695 AA.
XX
AC   AAU07207;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human beta-amyloid protein precursor, APP695-VF.
XX
KW   Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW   aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW   beta-secretase; Alzheimer's disease; APP695-VF.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 642
FT                   /note= "Wild type Val substituted by Phe"
XX
PN   WO200149097-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB000797.
XX
PR   09-MAY-2001; 2001WO-IB000797.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-502548/55.
DR   N-PSDB; AAS11707.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity.
XX
PS   Example 8; Page 141-143; 185pp; English.
XX
CC   The invention relates to a novel purified polypeptide comprising a
CC   fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC   Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC   and the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. Also included is an isoform of amyloid protein precursor (APP)
CC   comprising the amino acid sequence of a APP or its fragment containing an
CC   APP cleavage site recognisable by a mammalian beta-secretase, and further
CC   comprising two lysine residues at the carboxyl terminus of the amino acid
CC   sequence of the mammalian APP or APP fragment. The polypeptides are used
CC   for assaying for modulators of beta-secretase activity; identifying
CC   agents that inhibit the APP processing activity of human Asp2 aspartyl
CC   protease (Hu-Asp2); identifying agents that modulate the activity of Asp2
CC   ; and for reducing cellular production of amyloid beta (Abeta) from APP.
CC   Agents identified by the above methods are useful for treating
CC   Alzheimer's disease; and for identifying modulators of amyloid-beta
CC   (Abeta) peptide production, for use in designing therapeutics for the
CC   treatment or prevention of Alzheimer's disease. Probes and primers
CC   derived from Asp nucleic acid sequences are useful for detecting Hu-Asp
CC   nucleic acids in in vitro assays and in Northern and Southern blots. The
CC   present sequence represents the amino acid sequence of human amyloid
CC   protein precursor, APP695-VF, the coding sequence of which was used to
CC   prepare APP695-VF-KK (see AAS11710 and AAU07210) used in the method of
CC   the invention
XX
SQ   Sequence 695 AA;

  Query Match             66.0%;  Score 163;  DB 4;  Length 695;
  Best Local Similarity   70.8%;  Pred. No. 9.5e-14;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
              |||||||||||||||||||||||||||||||   |  : | :|  | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642


RESULT 9
AAE10634
ID   AAE10634 standard; protein; 695 AA.
XX
AC   AAE10634;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human amyloid protein precursor 695-VF (APP695-VF) isoform.
XX
KW   Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP695-VF;
KW   Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW   amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 642
FT                   /note= "Wild-type Val substituted with Phe"
XX
PN   GB2357767-A.
XX
PD   04-JUL-2001.
XX
PF   22-SEP-2000; 2000GB-00023315.
XX
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowski MJ,  Gurney M;
XX
DR   WPI; 2001-444208/48.
DR   N-PSDB; AAD17870.
XX
PT   Polypeptide comprising fragments of human aspartyl protease with amyloid
PT   precursor protein processing activity and alpha-secretase activity, for
PT   identifying modulators useful in treating Alzheimer's disease.
XX
PS   Example 8; Page 111-113; 187pp; English.
XX
CC   The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC   proteins which lack transmembrane domain or amino terminal domain or
CC   cytoplasmic domain and retains alpha-secretase activity and amyloid
CC   protein precursor (APP) processing activity. The proteins of the
CC   invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC   in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC   activity, where modulators that increase hu-Asp1 alpha-secretase activity
```

CC are useful for treating Alzheimer's disease (AD) which causes progressive
CC dementia with consequent formation of amyloid plaques, neurofibrillary
CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
CC with the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is human amyloid
CC protein precursor 695-VF (APP695-VF) isoform which is obtained by London
CC mutation in APP695 where Val at position 642 is replaced with Phe. APP695
CC -VF isoform is useful for assaying the beta-secretase activity of human
CC aspartyl protease 2a (hu-Asp2a) protein
XX
SQ Sequence 695 AA;

Query Match 66.0%; Score 163; DB 4; Length 695;
Best Local Similarity 70.8%; Pred. No. 9.5e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642

RESULT 10
AAE06864
ID AAE06864 standard; protein; 695 AA.
XX
AC AAE06864;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human amyloid precursor protein 695-VF (APP695-VF) isoform.
XX
KW Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-VF;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
KW neuroprotective; antisense therapy; gene therapy; APP695-VF; mutant;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 642
FT /note= "Wild type Val substituted with Phe"
XX
PN WO200150829-A2.
XX
PD 19-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB000799.
XX
PR 09-MAY-2001; 2001WO-IB000799.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-483072/52.
DR N-PSDB; AAD13026.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Example 8; Page 141-143; 185pp; English.
XX
CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-
CC Asp nucleic acids in in vitro assays and in Northern and Southern blots.
CC The present sequence is modified human amyloid precursor protein 695-VF
CC (APP695-VF) isoform. APP695-VF isoform is obtained by London V-F
CC mutation, where Val at position 642 is replaced with Phe. APP695-VF
CC isoform is useful for assaying the beta-secretase activity of human
CC aspartyl protease 2a (Hu-Asp2a) protein
XX
SQ Sequence 695 AA;

Query Match 66.0%; Score 163; DB 4; Length 695;
Best Local Similarity 70.8%; Pred. No. 9.5e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642

RESULT 11
AAE02586
ID AAE02586 standard; protein; 695 AA.
XX
AC AAE02586;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human amyloid precursor protein 695-VF (APP695-VF).
XX
KW Human; alpha-secretase; amyloid precursor protein 695-VF; APP695-VF;
KW therapy; Alzheimer's disease; antialzheimer's.
XX
OS Homo sapiens.
XX
PN WO200123533-A2.
XX
PD 05-APR-2001.
XX
PF 22-SEP-2000; 2000WO-US026080.
XX
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney M, Bienkowski MJ;
XX
DR WPI; 2001-290516/30.
DR N-PSDB; AAD06744.
XX
PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease.
XX
PS Example 8; Page 140-142; 189pp; English.
XX
CC The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of

```
CC   Alzheimer's disease. The present sequence is human APP695-VF. This
CC   sequence is characterised by a V to F alteration at position 642
XX
SQ   Sequence 695 AA;

  Query Match             66.0%;  Score 163;  DB 4;  Length 695;
  Best Local Similarity   70.8%;  Pred. No. 9.5e-14;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
              |||||||||||||||||||||||||||||||   |  : | :|  | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642


RESULT 12
AAU06608
ID   AAU06608 standard; protein; 695 AA.
XX
AC   AAU06608;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human Amyloid precursor protein mutant, APP695-VF.
XX
KW   Human; Aspartyl protease; Asp2b; beta-secretase; nootropic;
KW   neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW   amyloid-beta; Abeta; APP695-VF; London mutant; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 642
FT                   /note= "Wild-type Val substituted by Phe"
XX
PN   WO200149098-A2.
XX
PD   12-JUL-2001.
XX
PF   09-MAY-2001; 2001WO-IB000798.
XX
PR   09-MAY-2001; 2001WO-IB000798.
XX
PA   (BIEN/) BIENKOWSKI M J.
PA   (GURN/) GURNEY M E.
PA   (HEIN/) HEINRIKSON R L.
PA   (PARO/) PARODI L A.
PA   (YANR/) YAN R.
XX
PI   Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR   WPI; 2001-502549/55.
DR   N-PSDB; AAS11522.
XX
PT   Novel purified polypeptide comprising fragment of mammalian aspartyl
PT   protease 2, lacking Asp2 transmembrane domain and retaining beta
PT   secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT   activity.
XX
PS   Example 8; Page 141-143; 185pp; English.
XX
CC   The invention relates to a purified polypeptide comprising a fragment of
CC   mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC   transmembrane domain and the Asp2 protein, and where the polypeptide and
CC   the fragment retain the beta-secretase activity of the mammalian Asp2
CC   protein. The invention also details polynucleotides for the Asp proteins
CC   and vectors expressing them, and a polypeptide (isoform of amyloid
CC   protein precursor (APP)) comprising the amino acid sequence of an APP or
CC   its fragment containing an APP cleavage site recognizable by a mammalian
CC   beta-secretase, and further comprising two lysine residues at the
CC   carboxyl terminus of the amino acid sequence of the mammalian APP or APP
CC   fragment. Also included in the invention are methods of identifying
CC   modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC   useful for treating Alzheimer's disease. APP is useful in methods for
CC   identifying inhibitors or modulators of human Asp2 activity and amyloid-
CC   beta (Abeta) peptide production. APP is also useful in designing
CC   therapeutics for the treatment or prevention of Alzheimer's disease. APP
CC   comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is
CC   associated with increased levels of Abeta processing is useful in assays
CC   relating the Alzheimer's research. The expression vector is useful for
CC   recombinantly expressing APP. Nucleic acids that hybridise to Asp
CC   oligonucleotides are useful as probes or primers. The probes are useful
CC   for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
CC   Southern blots. The present sequence is the human APP695 mutant, APP695-
CC   VF (the London mutation). The mutation alters the specificity of the APP
CC   gamma-secretase activity and increases the rate of processing of the
CC   amyloid Abeta peptide
XX
SQ   Sequence 695 AA;

  Query Match             66.0%;  Score 163;  DB 4;  Length 695;
  Best Local Similarity   70.8%;  Pred. No. 9.5e-14;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
              |||||||||||||||||||||||||||||||   |  : | :|  | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642


RESULT 13
ABB78595
ID   ABB78595 standard; protein; 695 AA.
XX
AC   ABB78595;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human APP695-VF protein sequence SEQ ID NO:14.
XX
KW   Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic;
KW   amyloid precursor protein; APP.
XX
OS   Homo sapiens.
XX
PN   GB2367060-A.
XX
PD   27-MAR-2002.
XX
PF   29-OCT-2001; 2001GB-00025934.
XX
PR   23-SEP-1999;   99US-00404133.
PR   23-SEP-1999;   99US-0155493P.
PR   23-SEP-1999;   99WO-US020881.
PR   13-OCT-1999;   99US-00416901.
PR   06-DEC-1999;   99US-0169232P.
PR   22-SEP-2000; 2000GB-00023315.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Bienkowkski MJ,  Gurney M;
XX
DR   WPI; 2002-397167/43.
DR   N-PSDB; ABL52462.
XX
PT   Human aspartyl protease 1 substrates useful in assays to detect aspartyl
PT   protease activity, e.g. for the diagnosis of Alzheimer's disease.
XX
PS   Example 8; Page 111-113; 182pp; English.
XX
CC   The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC   substrate (I) which comprises a peptide of no more than 50 amino acids,
CC   and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC   Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC   proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC   (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC   proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC   nucleotide sequence that hybridises under stringent conditions to the non
```

CC -coding strand complementary to a defined 1804 nucleotide sequence (see
CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain); (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence represents human amyloid precursor protein APP695-VF, which is
CC given in an example from the present invention
XX
SQ Sequence 695 AA;

Query Match 66.0%; Score 163; DB 5; Length 695;
Best Local Similarity 70.8%; Pred. No. 9.5e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642

RESULT 14
AAY88430
ID AAY88430 standard; protein; 697 AA.
XX
AC AAY88430;
XX
DT 03-AUG-2000 (first entry)
XX
DE Human APP695-VF-KK amino acid sequence.
XX
KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW Alzheimer's disease; beta secretase site; APP695-VF-KK.
XX
OS Homo sapiens.
XX
PN WO200017369-A2.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-US020881.
XX
PR 24-SEP-1998; 98US-0101594P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2000-303209/26.
DR N-PSDB; AAA15667.
XX
PT New enzyme designated human aspartase useful in research into Alzheimer's
PT Disease is capable of cleaving amyloid protein precursor at the beta
PT secretase site to produce amyloid beta peptide.
XX
PS Claim 133; Page 148-153; 183pp; English.
XX
CC This sequence represents a modified version of the human amyloid
CC precursor protein (APP) amino acid sequence. The sequence is used in an
CC example of the method of the invention, to show that modification of APP
CC increases beta amyloid protein processing. The invention relates to a
CC protease (e.g. Asp2) capable of cleaving the beta secretase site of
CC amyloid precursor protein (APP). The protease contains a sequence
CC encoding the amino acid sequence DTG and a sequence encoding DSG or DTG
CC separated by 100-300 amino acids. When mutated the APP gene causes an
CC autosomal dominant form of Alzheimer's disease. APP localises to the cell
CC surface membrane and have a single C-terminal transmembrane domain.
CC Proteolytic processing of APP produces the amyloid beta protein, which is
CC possibly very important in Alzheimer's disease. The invention includes a
CC nucleotide sequence encoding the protease, a vector containing the
CC nucleotide sequence, and a cell line comprising the vector. Methods for
CC screening for inhibitors of beta secretase activity are also given in the
CC invention. The human aspartase protein and nucleotide sequences and the
CC methods for identifying inhibitors of the protease, are useful in the
CC treatment of and research in to Alzheimer's disease
XX
SQ Sequence 697 AA;

Query Match 66.0%; Score 163; DB 3; Length 697;
Best Local Similarity 70.8%; Pred. No. 9.5e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642

RESULT 15
AAU07210
ID AAU07210 standard; protein; 697 AA.
XX
AC AAU07210;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human beta-amyloid protein precursor, APP695-VF-KK.
XX
KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW beta-secretase; Alzheimer's disease; APP695-VF-KK.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 642
FT /note= "Wild type Val substituted by Phe"
XX
PN WO200149097-A2.
XX
PD 12-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB000797.
XX
PR 09-MAY-2001; 2001WO-IB000797.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-502548/55.
DR N-PSDB; AAS11710.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Example 8; Page 150-152; 185pp; English.
XX
CC The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing an

CC APP cleavage site recognisable by a mammalian beta-secretase, and further
CC comprising two lysine residues at the carboxyl terminus of the amino acid
CC sequence of the mammalian APP or APP fragment. The polypeptides are used
CC for assaying for modulators of beta-secretase activity; identifying
CC agents that inhibit the APP processing activity of human Asp2 aspartyl
CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2
CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.
CC Agents identified by the above methods are useful for treating
CC Alzheimer's disease; and for identifying modulators of amyloid-beta
CC (Abeta) peptide production, for use in designing therapeutics for the
CC treatment or prevention of Alzheimer's disease. Probes and primers
CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp
CC nucleic acids in in vitro assays and in Northern and Southern blots. The
CC present sequence represents the amino acid sequence of human amyloid
CC protein precursor, APP695-VF-KK, used in the method of the invention
XX
SQ Sequence 697 AA;

Query Match 66.0%; Score 163; DB 4; Length 697;
Best Local Similarity 70.8%; Pred. No. 9.5e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

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              ||||||||||||||||||||||||||||||    |  : | :|  | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642
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Search completed: June 18, 2004, 19:58:53
Job time : 70.2025 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:54:46 ; Search time 18.8466 Seconds
(without alignments)
131.485 Million cell updates/sec

Title: US-09-865-294A-74
Perfect score: 247
Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....KISITEIKGVIVHRIETILF 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	163	66.0	695	4	US-09-548-372D-14	Sequence 14, Appl
2	163	66.0	695	4	US-09-548-367D-14	Sequence 14, Appl
3	163	66.0	695	4	US-09-551-853D-14	Sequence 14, Appl
4	163	66.0	697	4	US-09-548-372D-20	Sequence 20, Appl
5	163	66.0	697	4	US-09-548-367D-20	Sequence 20, Appl
6	163	66.0	697	4	US-09-551-853D-20	Sequence 20, Appl
7	161.5	65.4	42	1	US-08-268-348A-6	Sequence 6, Appli
8	158.5	64.2	42	1	US-08-268-348A-5	Sequence 5, Appli
9	157.5	63.8	695	1	US-08-339-152A-30	Sequence 30, Appl
10	157	63.6	47	2	US-08-609-090-10	Sequence 10, Appl
11	157	63.6	48	4	US-09-560-883-1	Sequence 1, Appli
12	157	63.6	52	2	US-08-609-090-11	Sequence 11, Appl
13	157	63.6	53	3	US-09-173-887-5	Sequence 5, Appli
14	157	63.6	53	4	US-09-797-543-5	Sequence 5, Appli
15	157	63.6	59	1	US-08-484-969-3	Sequence 3, Appli
16	157	63.6	59	1	US-08-472-627-3	Sequence 3, Appli
17	157	63.6	59	1	US-08-388-463-3	Sequence 3, Appli
18	157	63.6	63	1	US-08-462-859A-4	Sequence 4, Appli
19	157	63.6	63	1	US-08-123-659A-4	Sequence 4, Appli
20	157	63.6	63	1	US-08-464-247A-4	Sequence 4, Appli
21	157	63.6	63	1	US-08-464-248A-4	Sequence 4, Appli
22	157	63.6	99	2	US-08-422-333-3	Sequence 3, Appli
23	157	63.6	99	3	US-08-339-708A-4	Sequence 4, Appli
24	157	63.6	99	3	US-08-339-708A-8	Sequence 8, Appli
25	157	63.6	100	6	5187153-10	Patent No. 5187153
26	157	63.6	100	6	5220013-10	Patent No. 5220013
27	157	63.6	100	6	5223482-10	Patent No. 5223482
28	157	63.6	103	2	US-08-404-831-2	Sequence 2, Appli
29	157	63.6	103	2	US-08-612-785B-2	Sequence 2, Appli
30	157	63.6	103	2	US-08-475-579A-2	Sequence 2, Appli
31	157	63.6	103	2	US-08-920-162A-2	Sequence 2, Appli
32	157	63.6	103	3	US-08-339-708A-10	Sequence 10, Appl
33	157	63.6	103	3	US-08-339-708A-12	Sequence 12, Appl
34	157	63.6	103	3	US-09-356-931-2	Sequence 2, Appli
35	157	63.6	103	4	US-08-703-675C-2	Sequence 2, Appli
36	157	63.6	103	4	US-08-617-267C-2	Sequence 2, Appli
37	157	63.6	103	4	US-09-519-019A-2	Sequence 2, Appli
38	157	63.6	105	2	US-08-729-345-1	Sequence 1, Appli
39	157	63.6	117	2	US-08-729-345-3	Sequence 3, Appli
40	157	63.6	117	4	US-09-422-569-10	Sequence 10, Appl
41	157	63.6	264	1	US-07-990-893-5	Sequence 5, Appli
42	157	63.6	487	1	US-08-462-859A-9	Sequence 9, Appli
43	157	63.6	487	1	US-08-123-659A-9	Sequence 9, Appli
44	157	63.6	487	1	US-08-464-247A-9	Sequence 9, Appli
45	157	63.6	487	1	US-08-464-248A-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-548-372D-14
; Sequence 14, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-14

Query Match 66.0%; Score 163; DB 4; Length 695;
Best Local Similarity 70.8%; Pred. No. 4e-15;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

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Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
              |||||||||||||||||||||||||||||    | : | :|  | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642
```

RESULT 2
US-09-548-367D-14
; Sequence 14, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-14

Query Match 66.0%; Score 163; DB 4; Length 695;
Best Local Similarity 70.8%; Pred. No. 4e-15;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642

RESULT 3
US-09-551-853D-14
; Sequence 14, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-14

Query Match 66.0%; Score 163; DB 4; Length 695;
Best Local Similarity 70.8%; Pred. No. 4e-15;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642

RESULT 4
US-09-548-372D-20
; Sequence 20, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-20

Query Match 66.0%; Score 163; DB 4; Length 697;
Best Local Similarity 70.8%; Pred. No. 4e-15;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642

RESULT 5
US-09-548-367D-20
; Sequence 20, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-20

Query Match 66.0%; Score 163; DB 4; Length 697;
Best Local Similarity 70.8%; Pred. No. 4e-15;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642

RESULT 6
US-09-551-853D-20
; Sequence 20, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881

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;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: US 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 697
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-551-853D-20

  Query Match             66.0%;  Score 163;  DB 4;  Length 697;
  Best Local Similarity   70.8%;  Pred. No. 4e-15;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
              |||||||||||||||||||||||||||||    |  : | :|  | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642


RESULT 7
US-08-268-348A-6
; Sequence 6, Application US/08268348A
; Patent No. 5750374
;  GENERAL INFORMATION:
;    APPLICANT:  Dobeli, Heinz
;    APPLICANT:  Draeger, Nicholas
;    APPLICANT:  Trottman, Gerda H
;    APPLICANT:  Jakob, Peter
;    APPLICANT:  Stuber, Dietrich
;    TITLE OF INVENTION:  Process for Producing Hydrophobic
;    TITLE OF INVENTION:  Polypeptides and Proteins, and Fusion Proteins for Use in
;    TITLE OF INVENTION:  Producing Same
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/268,348A
;      FILING DATE:  29-JUN-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93110755.1
;      FILING DATE:  06-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parise, John P.
;      REGISTRATION NUMBER:  34,403
;      REFERENCE/DOCKET NUMBER:  4105/157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-6326
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  42 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  N-terminal
US-08-268-348A-6

  Query Match             65.4%;  Score 161.5;  DB 1;  Length 42;
  Best Local Similarity   78.0%;  Pred. No. 1.8e-16;
  Matches   32;  Conservative    3;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISI-TEIKGVIV 40
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Db          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLEVGGVVI 41


RESULT 8
US-08-268-348A-5
; Sequence 5, Application US/08268348A
; Patent No. 5750374
;  GENERAL INFORMATION:
;    APPLICANT:  Dobeli, Heinz
;    APPLICANT:  Draeger, Nicholas
;    APPLICANT:  Trottman, Gerda H
;    APPLICANT:  Jakob, Peter
;    APPLICANT:  Stuber, Dietrich
;    TITLE OF INVENTION:  Process for Producing Hydrophobic
;    TITLE OF INVENTION:  Polypeptides and Proteins, and Fusion Proteins for Use in
;    TITLE OF INVENTION:  Producing Same
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/268,348A
;      FILING DATE:  29-JUN-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93110755.1
;      FILING DATE:  06-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parise, John P.
;      REGISTRATION NUMBER:  34,403
;      REFERENCE/DOCKET NUMBER:  4105/157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-6326
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  42 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  N-terminal
US-08-268-348A-5

  Query Match             64.2%;  Score 158.5;  DB 1;  Length 42;
  Best Local Similarity   75.6%;  Pred. No. 4.8e-16;
  Matches   31;  Conservative    4;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISI-TEIKGVIV 40
              |||||||||||||||||||||||||||||    |  :: ||::
Db          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLQVGGVVI 41


RESULT 9
US-08-339-152A-30
; Sequence 30, Application US/08339152A
; Patent No. 5643726
;  GENERAL INFORMATION:
;    APPLICANT:  Tanzi, Rudolph E.
;    APPLICANT:  Kovacs, Dora M.
;    TITLE OF INVENTION:  Methods For Modulating Transcription
;    TITLE OF INVENTION:  From The Amyloid  -Protein Precursor (APP) Promoter
;    NUMBER OF SEQUENCES:  33
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```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Ave., NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/339,152A
;      FILING DATE:  10-NOV-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  0609.4120000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  695 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-339-152A-30

  Query Match             63.8%;  Score 157.5;  DB 1;  Length 695;
  Best Local Similarity   68.1%;  Pred. No. 2.5e-14;
  Matches   32;  Conservative    4;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISI-TEIKGVIVHRIETI 46
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Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLNVGGVVIATVIVI 643


RESULT 10
US-08-609-090-10
; Sequence 10, Application US/08609090
; Patent No. 5840838
;  GENERAL INFORMATION:
;    APPLICANT:  HENSLEY, Kenneth
;    APPLICANT:  BUTTERFIELD, D. A.
;    APPLICANT:  CARNEY, John M.
;    APPLICANT:  AKSENOV, Michael
;    TITLE OF INVENTION:  A PROCESS FOR ENHANCING THE ACTIVITY OF
;    TITLE OF INVENTION:  AN OLIGOPEPTIDE OR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LOWE PRICE LEBLANC & BECKER
;      STREET:  99 Canal Center Plaza, Suite 300
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/609,090
;      FILING DATE:  29-FEB-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kraus, Eric J.
;      REGISTRATION NUMBER:  36,190
;      REFERENCE/DOCKET NUMBER:  434-059
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-684-1111
;      TELEFAX:  703-684-1124
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  47 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-609-090-10

  Query Match             63.6%;  Score 157;  DB 2;  Length 47;
  Best Local Similarity   70.2%;  Pred. No. 9.2e-16;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
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Db          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 45


RESULT 11
US-09-560-883-1
; Sequence 1, Application US/09560883
; Patent No. 6638711
; GENERAL INFORMATION:
;  APPLICANT:  Bush, Ashley
;  APPLICANT:  Huang, Xudong
;  APPLICANT:  Atwood, Craig
;  APPLICANT:  Tanzi, Rudolph
;  TITLE OF INVENTION:  Method of Screening for Drugs Useful in Treating Alzheimer's D
;  FILE REFERENCE:  0609.4810001/REF/KKV
;  CURRENT APPLICATION NUMBER:  US/09/560,883
;  CURRENT FILING DATE:  2000-04-28
;  PRIOR APPLICATION NUMBER:  09/380,704
;  PRIOR FILING DATE:  1999-09-08
;  PRIOR APPLICATION NUMBER:  PCT/US98/04683
;  PRIOR FILING DATE:  1998-03-11
;  PRIOR APPLICATION NUMBER:  08/816,122
;  PRIOR FILING DATE:  1997-03-11
;  NUMBER OF SEQ ID NOS:  1
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 1
;  LENGTH: 48
;  TYPE: PRT
;  ORGANISM: Human amyloid protein precursor
;  FEATURE:
;  NAME/KEY: PEPTIDE
;  LOCATION: (4)..(45)
;  OTHER INFORMATION: A beta
US-09-560-883-1

  Query Match             63.6%;  Score 157;  DB 4;  Length 48;
  Best Local Similarity   70.2%;  Pred. No. 9.5e-16;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||||||||||||||||||||||||||||    |  : | :|  | |::
Db          4 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 48


RESULT 12
US-08-609-090-11
; Sequence 11, Application US/08609090
; Patent No. 5840838
;  GENERAL INFORMATION:
;    APPLICANT:  HENSLEY, Kenneth
;    APPLICANT:  BUTTERFIELD, D. A.
;    APPLICANT:  CARNEY, John M.
;    APPLICANT:  AKSENOV, Michael
;    TITLE OF INVENTION:  A PROCESS FOR ENHANCING THE ACTIVITY OF
;    TITLE OF INVENTION:  AN OLIGOPEPTIDE OR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  LOWE PRICE LEBLANC & BECKER
;       STREET:  99 Canal Center Plaza, Suite 300
;       CITY:  Alexandria
;       STATE:  Virginia
;       COUNTRY:  USA
;       ZIP:  22314
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/609,090
;       FILING DATE:  29-FEB-1996
;       CLASSIFICATION:  530
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kraus, Eric J.
;       REGISTRATION NUMBER:  36,190
;       REFERENCE/DOCKET NUMBER:  434-059
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  703-684-1111
;       TELEFAX:  703-684-1124
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  52 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-609-090-11

  Query Match             63.6%;  Score 157;  DB 2;  Length 52;
  Best Local Similarity   70.2%;  Pred. No. 1e-15;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

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              ||||||||||||||||||||||||||||    |  : | :|  | |::
Db          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 45


RESULT 13
US-09-173-887-5
; Sequence 5, Application US/09173887
; Patent No. 6245884
; GENERAL INFORMATION:
;  APPLICANT: Hook, Vivian Y.H.
;  TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA
;  FILE REFERENCE: P-AS 3337
;  CURRENT APPLICATION NUMBER: US/09/173,887
;  CURRENT FILING DATE: 1998-10-16
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 53
;   TYPE: PRT
;   ORGANISM: mammalian
US-09-173-887-5

  Query Match             63.6%;  Score 157;  DB 3;  Length 53;
  Best Local Similarity   70.2%;  Pred. No. 1.1e-15;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              ||||||||||||||||||||||||||||    |  : | :|  | |::
Db          4 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 48


RESULT 14
US-09-797-543-5
; Sequence 5, Application US/09797543
; Patent No. 6627409
; GENERAL INFORMATION:
;  APPLICANT: Hook, Vivian Y.H.
;  TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA
;  FILE REFERENCE: P-AS 4579
;  CURRENT APPLICATION NUMBER: US/09/797,543
;  CURRENT FILING DATE:  2001-05-29
;  PRIOR APPLICATION NUMBER: US 09/173,887
;  PRIOR FILING DATE: 1998-10-16
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 53
;   TYPE: PRT
;   ORGANISM: 'Axial Seamount' polynoid polychaete
US-09-797-543-5

  Query Match             63.6%;  Score 157;  DB 4;  Length 53;
  Best Local Similarity   70.2%;  Pred. No. 1.1e-15;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
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Db          4 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 48


RESULT 15
US-08-484-969-3
; Sequence 3, Application US/08484969
; Patent No. 5679531
;  GENERAL INFORMATION:
;    APPLICANT:  Konig, Gerhard
;    APPLICANT:  Graham, Paul
;    TITLE OF INVENTION:  Monoclonal Antibody Specific for BA4
;    TITLE OF INVENTION:  Peptide
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 South Wacker Drive Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,969
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDonnell, John J
;      REGISTRATION NUMBER:  26,949
;      REFERENCE/DOCKET NUMBER:  95,216
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  59 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Cleavage-site
;      LOCATION:  4..5
;      OTHER INFORMATION:  /label= Beta
;      OTHER INFORMATION:  /note= "Beta cleavage site in APP"
;    FEATURE:
;      NAME/KEY:  Cleavage-site
;      LOCATION:  20..21
;      OTHER INFORMATION:  /label= Alpha
;      OTHER INFORMATION:  /note= "Alpha cleavage site in APP, residues 16/17
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;   FEATURE:
;     NAME/KEY:  Cleavage-site
;     LOCATION:  46..47
;     OTHER INFORMATION:  /label= Gamma
;     OTHER INFORMATION:  /note= "Gamma cleavage site in APP"
;   FEATURE:
;     NAME/KEY:  Peptide
;     LOCATION:  5..47
;     OTHER INFORMATION:  /label= BA4
;     OTHER INFORMATION:  /note= "BA4 peptide"
;   FEATURE:
;     NAME/KEY:  Region
;     LOCATION:  33..56
;     OTHER INFORMATION:  /label= Tm
;     OTHER INFORMATION:  /note= "Transmembrane region of APP"
;   FEATURE:
;     NAME/KEY:  Region
;     LOCATION:  1..32
;     OTHER INFORMATION:  /label= Ex
;     OTHER INFORMATION:  /note= "N-terminal extracellular part of APP"
US-08-484-969-3

  Query Match             63.6%;  Score 157;  DB 1;  Length 59;
  Best Local Similarity   70.2%;  Pred. No. 1.2e-15;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
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Db          5 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 49


Search completed: June 18, 2004, 20:04:46
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 20:02:36 ; Search time 54.1841 Seconds
(without alignments)
250.093 Million cell updates/sec

Title: US-09-865-294A-74
Perfect score: 247
Sequence: 1 DAEFRHDSGYEVHHQKLVFP.....KISITEIKGVIVHRIETILF 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	247	100.0	48	10	US-09-865-294-74	Sequence 74, Appl
2	163	66.0	100	15	US-10-275-025-5	Sequence 5, Appli
3	163	66.0	108	15	US-10-275-025-13	Sequence 13, Appl
4	163	66.0	695	9	US-09-794-927-14	Sequence 14, Appl
5	163	66.0	695	9	US-09-795-847-14	Sequence 14, Appl
6	163	66.0	695	9	US-09-794-743-14	Sequence 14, Appl
7	163	66.0	695	9	US-09-794-748-14	Sequence 14, Appl
8	163	66.0	695	9	US-09-794-925-14	Sequence 14, Appl
9	163	66.0	695	9	US-09-681-442-14	Sequence 14, Appl
10	163	66.0	695	10	US-09-869-414-14	Sequence 14, Appl
11	163	66.0	695	10	US-09-548-366-14	Sequence 14, Appl
12	163	66.0	695	12	US-10-652-927-14	Sequence 14, Appl
13	163	66.0	695	12	US-10-652-830-14	Sequence 14, Appl
14	163	66.0	697	9	US-09-794-927-20	Sequence 20, Appl
15	163	66.0	697	9	US-09-795-847-20	Sequence 20, Appl
16	163	66.0	697	9	US-09-794-743-20	Sequence 20, Appl
17	163	66.0	697	9	US-09-794-748-20	Sequence 20, Appl
18	163	66.0	697	9	US-09-794-925-20	Sequence 20, Appl
19	163	66.0	697	9	US-09-681-442-20	Sequence 20, Appl
20	163	66.0	697	10	US-09-869-414-20	Sequence 20, Appl
21	163	66.0	697	10	US-09-548-366-20	Sequence 20, Appl
22	163	66.0	697	12	US-10-652-927-20	Sequence 20, Appl
23	163	66.0	697	12	US-10-652-830-20	Sequence 20, Appl
24	160	64.8	34	10	US-09-865-294-73	Sequence 73, Appl
25	157	63.6	53	9	US-09-797-543-5	Sequence 5, Appli
26	157	63.6	53	13	US-10-016-717-1	Sequence 1, Appli
27	157	63.6	70	9	US-09-155-076-14	Sequence 14, Appl
28	157	63.6	82	10	US-09-848-616-173	Sequence 173, App
29	157	63.6	82	14	US-10-050-902-219	Sequence 219, App
30	157	63.6	82	14	US-10-050-898-219	Sequence 219, App
31	157	63.6	99	14	US-10-183-119-2	Sequence 2, Appli
32	157	63.6	100	9	US-09-794-975-4	Sequence 4, Appli
33	157	63.6	100	15	US-10-275-025-1	Sequence 1, Appli
34	157	63.6	100	15	US-10-275-025-3	Sequence 3, Appli
35	157	63.6	100	15	US-10-275-025-4	Sequence 4, Appli
36	157	63.6	103	9	US-09-972-475-2	Sequence 2, Appli
37	157	63.6	103	9	US-09-895-443-2	Sequence 2, Appli
38	157	63.6	103	15	US-10-395-290-2	Sequence 2, Appli
39	157	63.6	103	15	US-10-463-729-2	Sequence 2, Appli
40	157	63.6	108	15	US-10-275-025-9	Sequence 9, Appli
41	157	63.6	108	15	US-10-275-025-11	Sequence 11, Appl
42	157	63.6	108	15	US-10-275-025-12	Sequence 12, Appl
43	157	63.6	117	9	US-09-794-975-6	Sequence 6, Appli
44	157	63.6	117	9	US-09-823-153-2	Sequence 2, Appli
45	157	63.6	117	10	US-09-422-569-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-865-294-74
; Sequence 74, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; TITLE OF INVENTION: prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Measles virus
US-09-865-294-74

Query Match 100.0%; Score 247; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 5.1e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48

RESULT 2
US-10-275-025-5
; Sequence 5, Application US/10275025
; Publication No. US20030215896A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yueming
; APPLICANT: Xu, Min
; APPLICANT: Huang, Qian
; APPLICANT: Gardell, Stephen J.
; TITLE OF INVENTION: GAMMA SECRETASE SUBSTRATES AND IN VITRO

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;  TITLE OF INVENTION:  ASSAYS
;  FILE REFERENCE: 20507P
;  CURRENT APPLICATION NUMBER: US/10/275,025
;  CURRENT FILING DATE:  2002-10-31
;  PRIOR APPLICATION NUMBER: PCT/US01/13332
;  PRIOR FILING DATE: 2001-04-25
;  PRIOR APPLICATION NUMBER: 60/201,053
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 100
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Beta-CTF domain
US-10-275-025-5

  Query Match            66.0%;  Score 163;  DB 15;  Length 100;
  Best Local Similarity   70.8%;  Pred. No. 2.8e-14;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
              |||||||||||||||||||||||||||||    |  : | :|  | |::|
Db          2 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 47


RESULT 3
US-10-275-025-13
; Sequence 13, Application US/10275025
; Publication No. US20030215896A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Yueming
;  APPLICANT:  Xu, Min
;  APPLICANT:  Huang, Qian
;  APPLICANT:  Gardell, Stephen J.
;  TITLE OF INVENTION: GAMMA SECRETASE SUBSTRATES AND IN VITRO
;  TITLE OF INVENTION:  ASSAYS
;  FILE REFERENCE: 20507P
;  CURRENT APPLICATION NUMBER: US/10/275,025
;  CURRENT FILING DATE:  2002-10-31
;  PRIOR APPLICATION NUMBER: PCT/US01/13332
;  PRIOR FILING DATE: 2001-04-25
;  PRIOR APPLICATION NUMBER: 60/201,053
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Gamma-secretase substrate
US-10-275-025-13

  Query Match            66.0%;  Score 163;  DB 15;  Length 108;
  Best Local Similarity   70.8%;  Pred. No. 3e-14;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
              |||||||||||||||||||||||||||||    |  : | :|  | |::|
Db          2 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 47


RESULT 4
US-09-794-927-14
; Sequence 14, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280PG
;  CURRENT APPLICATION NUMBER: US/09/794,927
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-927-14

  Query Match            66.0%;  Score 163;  DB 9;  Length 695;
  Best Local Similarity   70.8%;  Pred. No. 2.7e-13;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
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Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642


RESULT 5
US-09-795-847-14
; Sequence 14, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280DE
;  CURRENT APPLICATION NUMBER: US/09/795,847
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-795-847-14

  Query Match            66.0%;  Score 163;  DB 9;  Length 695;
  Best Local Similarity   70.8%;  Pred. No. 2.7e-13;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
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Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642


RESULT 6
US-09-794-743-14
; Sequence 14, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280BC
;  CURRENT APPLICATION NUMBER: US/09/794,743
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-743-14

  Query Match             66.0%;  Score 163;  DB 9;  Length 695;
  Best Local Similarity   70.8%;  Pred. No. 2.7e-13;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
                ||||||||||||||||||||||||||||||    |  : | :|  | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642


RESULT 7
US-09-794-748-14
; Sequence 14, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280JL
;  CURRENT APPLICATION NUMBER: US/09/794,748
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-748-14

  Query Match             66.0%;  Score 163;  DB 9;  Length 695;
  Best Local Similarity   70.8%;  Pred. No. 2.7e-13;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
                ||||||||||||||||||||||||||||||    |  : | :|  | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642


RESULT 8
US-09-794-925-14
; Sequence 14, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USE
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  28341/6280HI
;  CURRENT APPLICATION NUMBER: US/09/794,925
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER:  09/416,901
;  PRIOR FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-794-925-14

  Query Match             66.0%;  Score 163;  DB 9;  Length 695;
  Best Local Similarity   70.8%;  Pred. No. 2.7e-13;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
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Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642


RESULT 9
US-09-681-442-14
; Sequence 14, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280FG
;  CURRENT APPLICATION NUMBER: US/09/681,442
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;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-681-442-14

  Query Match             66.0%;  Score 163;  DB 9;  Length 695;
  Best Local Similarity   70.8%;  Pred. No. 2.7e-13;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
              |||||||||||||||||||||||||||||   |  : | :|  | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642


RESULT 10
US-09-869-414-14
; Sequence 14, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
;  APPLICANT: Beinkowski et al.
;  TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 28341/6280M
;  CURRENT APPLICATION NUMBER: US/09/869,414
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-869-414-14

  Query Match             66.0%;  Score 163;  DB 10;  Length 695;
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  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
              |||||||||||||||||||||||||||||   |  : | :|  | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642


RESULT 11
US-09-548-366-14
; Sequence 14, Application US/09548366
; Publication No. US20030104365A1
; GENERAL INFORMATION:
;  APPLICANT:  Gurney, Mark E.
;  APPLICANT:  Bienkowski, Michael J.
;  APPLICANT:  Heinrikson, Robert L.
;  APPLICANT:  Parodi, Luis A.
;  APPLICANT:  Yan, Riqiang
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;  TITLE OF INVENTION:  USES THEREFOR
;  FILE REFERENCE:  28341/6280A
;  CURRENT APPLICATION NUMBER: US/09/548,366
;  CURRENT FILING DATE:  2000-04-12
;  PRIOR APPLICATION NUMBER:  60/155,493
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  09/404,133
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  PCT/US99/20881
;  PRIOR FILING DATE:  1999-09-23
;  PRIOR APPLICATION NUMBER:  60/101,594
;  PRIOR FILING DATE:  1998-09-24
;  NUMBER OF SEQ ID NOS:  65
;  SOFTWARE:  PatentIn Ver. 2.0
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;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-548-366-14

  Query Match             66.0%;  Score 163;  DB 10;  Length 695;
  Best Local Similarity   70.8%;  Pred. No. 2.7e-13;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
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Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642


RESULT 12
US-10-652-927-14
; Sequence 14, Application US/10652927
; Publication No. US20040043408A1
; GENERAL INFORMATION:
;  APPLICANT: Gurney et al.
;  TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
;  TITLE OF INVENTION:  Therefor
;  FILE REFERENCE: 29915/6280N3
;  CURRENT APPLICATION NUMBER: US/10/652,927
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: 09/794,925
;  PRIOR FILING DATE: 2001-02-27
;  PRIOR APPLICATION NUMBER: 09/416,901
;  PRIOR FILING DATE: 1999-10-13
;  PRIOR APPLICATION NUMBER: 60/155,493
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 09/404,133
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: PCT/US99/20881
;  PRIOR FILING DATE: 1999-09-23
;  PRIOR APPLICATION NUMBER: 60/101,594
;  PRIOR FILING DATE: 1998-09-24
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-652-927-14

  Query Match             66.0%;  Score 163;  DB 12;  Length 695;
  Best Local Similarity   70.8%;  Pred. No. 2.7e-13;
  Matches   34;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

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              |||||||||||||||||||||||||||||   |  : | :|  | |::|
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642
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RESULT 13
US-10-652-830-14
; Sequence 14, Application US/10652830
; Publication No. US20040048303A1
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 29915/6280N1
; CURRENT APPLICATION NUMBER: US/10/652,830
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 09/794,925
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-652-830-14

Query Match 66.0%; Score 163; DB 12; Length 695;
Best Local Similarity 70.8%; Pred. No. 2.7e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
||||||||||||||||||||||||||||| | : | :| | |::|
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642

RESULT 14
US-09-794-927-20
; Sequence 20, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-20

Query Match 66.0%; Score 163; DB 9; Length 697;
Best Local Similarity 70.8%; Pred. No. 2.7e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
||||||||||||||||||||||||||||| | : | :| | |::|
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642

RESULT 15
US-09-795-847-20
; Sequence 20, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-847-20

Query Match 66.0%; Score 163; DB 9; Length 697;
Best Local Similarity 70.8%; Pred. No. 2.7e-13;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
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Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 642

Search completed: June 18, 2004, 20:23:47
Job time : 54.1841 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:45 ; Search time 14.4294 Seconds
(without alignments)
319.984 Million cell updates/sec

Title: US-09-865-294A-74
Perfect score: 247
Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....KISITEIKGVIVHRIETILF 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	157	63.6	57	2	F60045	Alzheimer's diseas
3	157	63.6	57	2	G60045	Alzheimer's diseas
4	157	63.6	57	2	D60045	Alzheimer's diseas
5	157	63.6	57	2	A60045	Alzheimer's diseas
6	157	63.6	57	2	B60045	Alzheimer's diseas
7	157	63.6	82	2	PQ0438	Alzheimer's diseas
8	157	63.6	695	1	A49795	Alzheimer's diseas
9	157	63.6	770	1	QRHUA4	Alzheimer's diseas
10	155	62.8	42	2	PN0512	beta-amyloid prote
11	138	55.9	695	2	A27485	Alzheimer's diseas
12	138	55.9	695	2	S00550	Alzheimer's diseas
13	138	55.9	747	2	JH0773	Alzheimer's diseas
14	133	53.8	33	2	S23094	beta-amyloid prote
15	64	25.9	546	1	VGNZRL	cell fusion glycop
16	63.5	25.7	663	2	A86626	hypothetical prote
17	62	25.1	327	2	S11435	genome polyprotein
18	62	25.1	662	1	VGNZCD	cell fusion glycop
19	62	25.1	662	2	S21382	cell fusion protei
20	61	24.7	546	2	S47300	gene F protein - r
21	61	24.7	631	1	VGNZPD	cell fusion glycop
22	61	24.7	631	1	A48346	cell fusion glycop
23	60	24.3	546	1	VGNZRK	cell fusion glycop
24	60	24.3	546	2	S55386	cell fusion protei
25	60	24.3	546	2	S47305	gene F protein - r
26	60	24.3	3063	2	JS0166	genome polyprotein
27	59	23.9	284	2	S04723	genome polyprotein
28	59	23.9	542	2	JQ2223	cell fusion protei
29	59	23.9	552	2	S47034	cell fusion protei
30	58	23.5	282	2	PQ0376	cell fusion glycop
31	58	23.5	282	2	PQ0388	cell fusion glycop
32	58	23.5	534	1	JU0274	cell fusion glycop
33	58	23.5	550	1	E48556	cell fusion glycop
34	58	23.5	553	1	VGNZMV	cell fusion glycop
35	57	23.1	79	2	B90314	hypothetical prote
36	57	23.1	298	2	A90331	transposase in ISC
37	56.5	22.9	356	2	D96537	hypothetical prote
38	56.5	22.9	971	2	D70128	conserved hypothet
39	56	22.7	127	2	F90475	hypothetical prote
40	56	22.7	229	2	F86180	hypothetical prote
41	56	22.7	1328	2	B22999	TyB protein - yeas
42	55.5	22.5	247	2	A85688	hypothetical prote
43	55.5	22.5	274	2	C90830	probable replicati
44	55.5	22.5	323	2	T14719	partitioning prote
45	55.5	22.5	330	2	A26205	coat protein precu

ALIGNMENTS

RESULT 1
E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C;Species: Ovis sp. (sheep)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: E60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: E60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56130
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 63.6%; Score 157; DB 2; Length 57;
Best Local Similarity 70.2%; Pred. No. 3e-13;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

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Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||||||||||||||||||||||||||||    |  : | :|  | |::
Db          6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 50
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RESULT 2
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: F60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: F60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 63.6%; Score 157; DB 2; Length 57;
Best Local Similarity 70.2%; Pred. No. 3e-13;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

```
Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||||||||||||||||||||||||||||    |  : | :|  | |::
Db          6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 50
```

RESULT 3
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: G60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: G60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56126
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 63.6%; Score 157; DB 2; Length 57;
Best Local Similarity 70.2%; Pred. No. 3e-13;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 50

RESULT 4
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: D60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: D60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56124
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 63.6%; Score 157; DB 2; Length 57;
Best Local Similarity 70.2%; Pred. No. 3e-13;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 50

RESULT 5
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: A60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: A60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56125
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 63.6%; Score 157; DB 2; Length 57;
Best Local Similarity 70.2%; Pred. No. 3e-13;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 50

RESULT 6
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C;Species: Ursus maritimus (polar bear)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: B60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: B60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 63.6%; Score 157; DB 2; Length 57;
Best Local Similarity 70.2%; Pred. No. 3e-13;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 50

RESULT 7
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: PQ0438; C60045
R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A;Reference number: PQ0438; MUID:93075180; PMID:1445331
A;Accession: PQ0438
A;Molecule type: DNA
A;Residues: 1-82 <DAV>
A;Cross-references: GB:M83558; GB:M83657
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: C60045
A;Molecule type: mRNA
A;Residues: 12-68 <JOH>
A;Cross-references: EMBL:X56129
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 63.6%; Score 157; DB 2; Length 82;
Best Local Similarity 70.2%; Pred. No. 4.5e-13;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
Db 17 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 61

RESULT 8
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49795
R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991

A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a p
A;Reference number: A49795; MUID:91273117; PMID:1905108
A;Accession: A49795
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-695 <POD>
A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing

Query Match 63.6%; Score 157; DB 1; Length 695;
Best Local Similarity 70.2%; Pred. No. 4.5e-12;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 641

RESULT 9
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibi
N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44
4668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S3
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288,'V',365-770 <LEM1>
A;Cross-references: EMBL:X13466
A;Note: alternative splice form APP(695)
R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A;Note: alternative splice form APP(695)
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A;Reference number: A32277; MUID:89165870; PMID:2538123
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAF>
A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A;Reference number: A33260; MUID:89392030; PMID:2675837
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM
A;Molecule type: DNA
A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duin
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorr
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheim
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 689-716,'F',718-737 <MUR>
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692,'G',694-718 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfa
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288,'V',365-770 <KAN>
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987

A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756,'S',758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344,'I',365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344,'I',365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288,'V',365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 60
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 6
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K

  Query Match 63.6%; Score 157; DB 1; Length 770;
  Best Local Similarity 70.2%; Pred. No. 5.1e-12;
  Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
Db 672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 716

RESULT 10
PN0512
beta-amyloid protein - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PN0512
R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno,
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragm
A;Reference number: PN0512; MUID:93290653; PMID:7685598
A;Accession: PN0512
A;Molecule type: protein
A;Residues: 1-42 <SHI>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid

  Query Match 62.8%; Score 155; DB 2; Length 42;
  Best Local Similarity 77.5%; Pred. No. 3.9e-13;
  Matches 31; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIV 40
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

RESULT 11
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N;Alternate names: proteinase nexin II
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C;Accession: A27485; S19727; I49485
R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein prec
A;Reference number: A27485; MUID:88106489; PMID:3322280
A;Accession: A27485
A;Molecule type: mRNA
A;Residues: 1-695 <YAM>
A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A;Experimental source: brain
R;de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A;Reference number: S19727; MUID:92096458; PMID:1756177
A;Accession: S19727
A;Molecule type: mRNA
A;Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695 <STR>
A;Cross-references: EMBL:X59379
R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the Alzheimer'
A;Reference number: I49485; MUID:92209998; PMID:1555768
A;Accession: I49485
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>

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A;Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C;Genetics:
A;Map position: 16C3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; amyloid; transmembrane protein

  Query Match             55.9%;  Score 138;  DB 2;  Length 695;
  Best Local Similarity   63.8%;  Pred. No. 1.2e-09;
  Matches   30;  Conservative    5;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||| |||| :|| |||||||||||||||   |  : | :|  | |::
Db        597 DAEFGHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 641


RESULT 12
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A;Reference number: S00550; MUID:88312583; PMID:2900758
A;Accession: S00550
A;Molecule type: mRNA
A;Residues: 1-695 <SHI>
A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A;Reference number: A41245; MUID:88264430; PMID:2968652
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627; PMID:7913895
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brai
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is ch
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TMM>

  Query Match             55.9%;  Score 138;  DB 2;  Length 695;
  Best Local Similarity   63.8%;  Pred. No. 1.2e-09;
  Matches   30;  Conservative    5;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||| |||| :|| |||||||||||||||   |  : | :|  | |::
Db        597 DAEFGHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 641


RESULT 13
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match             55.9%;  Score 138;  DB 2;  Length 747;
  Best Local Similarity   59.6%;  Pred. No. 1.3e-09;
  Matches   28;  Conservative    8;  Mismatches    9;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |:|:|||: |||||||||||||:|||||   |  : | :|  | |::
Db        649 DSEYRHDTAYEVHHQKLVFFAEEVGSNKGAIIGLMVGGVV--IATVI 693


RESULT 14
S23094
beta-amyloid protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C;Accession: S23094
R;Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinas
A;Reference number: S23094; MUID:92316198; PMID:1618299
A;Accession: S23094
A;Molecule type: protein
A;Residues: 1-33 <KOJ>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

  Query Match             53.8%;  Score 133;  DB 2;  Length 33;
  Best Local Similarity   89.3%;  Pred. No. 2e-10;
  Matches   25;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNK 28
              |||| |||| :|| ||||||||||||||
Db          6 DAEFGHDSGFEVRHQKLVFFAEDVGSNK 33


RESULT 15
VGNZRL
cell fusion glycoprotein precursor - rinderpest virus (strain L)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: rinderpest virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Accession: A28921
R;Tsukiyama, K.; Yoshikawa, Y.; Yamanouchi, K.
Virology 164, 523-530, 1988
A;Title: Fusion glycoprotein (F) of rinderpest virus: entire nucleotide sequence of the
A;Reference number: A28921; MUID:88219541; PMID:3285575
A;Accession: A28921
A;Molecule type: mRNA
A;Residues: 1-546 <TSU>
A;Cross-references: GB:M20870; NID:g333898; PIDN:AAA47399.1; PID:g333899
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-104/Product: cell fusion glycoprotein F2 #status predicted <FG2>
F;105-546/Product: cell fusion glycoprotein F1 #status predicted <FG1>
F;109-133/Domain: transmembrane #status predicted <TN1>
F;485-513/Domain: transmembrane #status predicted <TN2>
F;25,57,63/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             25.9%;  Score 64;  DB 1;  Length 546;
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Best Local Similarity 61.1%; Pred. No. 3;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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Qy          31 SITEIKGVIVHRIETILF 48
               |::|||||||||:|:: :
Db         283 SLSEIKGVIVHRLESVSY 300
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Search completed: June 18, 2004, 20:03:31
Job time : 14.4294 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:49:55 ; Search time 9.42331 Seconds
(without alignments)
265.232 Million cell updates/sec

Title: US-09-865-294A-74
Perfect score: 247
Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....KISITEIKGVIVHRIETILF 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	157	63.6	57	1	A4_URSMA	Q29149 ursus marit
2	157	63.6	58	1	A4_CANFA	Q28280 canis famil
3	157	63.6	58	1	A4_RABIT	Q28748 oryctolagus
4	157	63.6	58	1	A4_SHEEP	Q28757 ovis aries
5	157	63.6	59	1	A4_BOVIN	Q28053 bos taurus
6	157	63.6	751	1	A4_SAISC	Q95241 s amyloid b
7	157	63.6	770	1	A4_CAVPO	Q60495 c amyloid b
8	157	63.6	770	1	A4_HUMAN	P05067 h amyloid b
9	157	63.6	770	1	A4_MACFA	P53601 m amyloid b
10	157	63.6	770	1	A4_PIG	P79307 s amyloid b
11	138	55.9	770	1	A4_MOUSE	P12023 m amyloid b
12	138	55.9	770	1	A4_RAT	P08592 r amyloid b
13	115	46.6	780	1	A4_TETFL	O73683 tetraodon f
14	111	44.9	737	1	A4_FUGRU	O93279 fugu rubrip
15	64	25.9	546	1	VGLF_RINDL	P10864 rinderpest
16	62	25.1	327	1	POLG_PVYCH	P21294 potato viru
17	62	25.1	662	1	VGLF_CDVO	P12569 canine dist
18	61	24.7	546	1	VGLF_RINDB	P41360 rinderpest
19	61	24.7	631	1	VGLF_PHODV	P28886 phocine dis
20	60	24.3	546	1	VGLF_RINDR	P41356 rinderpest
21	60	24.3	3063	1	POLG_PVYN	P18247 p genome po
22	59	23.9	284	1	POLG_PVYYO	P11897 potato viru
23	58	23.5	534	1	VGLF_MEASY	P26032 measles vir
24	58	23.5	550	1	VGLF_MEASA	P35973 measles vir
25	58	23.5	550	1	VGLF_MEASE	P08300 measles vir
26	57.5	23.3	506	1	MATK_ERITE	O47157 erica tetra
27	57	23.1	338	1	SYFA_FUSNN	Q8rhb4 fusobacteri
28	56.5	22.9	356	1	BCA6_ARATH	Q9lpm9 arabidopsis
29	56.5	22.9	971	1	Y228_BORBU	O51246 borrelia bu
30	56	22.7	229	1	V726_ARATH	Q9mas5 arabidopsis
31	56	22.7	506	1	MATK_RHOTS	O62991 rhododendro
32	55.5	22.5	330	1	COAT_PEMV	P07993 pepper mott
33	55.5	22.5	506	1	MATK_CALVU	O47143 calluna vul
34	55.5	22.5	1442	1	DPO3_UREPA	Q9pqb4 ureaplasma
35	55	22.3	220	1	V725_ARATH	O48850 arabidopsis
36	55	22.3	221	1	V714_ARATH	Q9fmr5 arabidopsis
37	55	22.3	240	1	V727_ARATH	Q9m376 arabidopsis
38	55	22.3	316	1	YMX1_CAEEL	P34509 caenorhabdi
39	54	21.9	321	1	RBSC_ECOLI	P04984 escherichia
40	54	21.9	546	1	VGLF_RINDK	P12574 rinderpest
41	53.5	21.7	430	1	PURA_LACLA	Q9ce93 lactococcus
42	53.5	21.7	518	1	OPGG_NITEU	Q82sa9 nitrosomona
43	53.5	21.7	708	1	YNZB_CAEEL	P45972 caenorhabdi
44	53.5	21.7	842	1	DP3A_THEMA	Q9zhg4 thermotoga
45	53	21.5	251	1	TPIS_XANCP	Q8p7t0 xanthomonas

ALIGNMENTS

RESULT 1
A4_URSMA
ID A4_URSMA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ursus maritimus (Polar bear) (Thalarctos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC ----------

CC ----------
DR EMBL; X56128; CAA39593.1; -.
DR PIR; B60045; B60045.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 63.6%; Score 157; DB 1; Length 57;
Best Local Similarity 70.2%; Pred. No. 1.4e-13;
Matches 33; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

```
Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              ||||||||||||||||||||||||||||||   |  : | :|  | |::
Db          6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 50


RESULT 2
A4_CANFA
ID   A4_CANFA       STANDARD;      PRT;    58 AA.
AC   Q28280;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56125; CAA39590.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     58       POTENTIAL.
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6285 MW;  8469D488A2E12DFA CRC64;

  Query Match             63.6%;  Score 157;  DB 1;  Length 58;
  Best Local Similarity   70.2%;  Pred. No. 1.5e-13;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              ||||||||||||||||||||||||||||||   |  : | :|  | |::
Db          7 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 51


RESULT 3
A4_RABIT
ID   A4_RABIT       STANDARD;      PRT;    58 AA.
AC   Q28748;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56129; CAA39594.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   DOMAIN       58    >58       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6300 MW;  F434209D88EBA82D CRC64;

  Query Match             63.6%;  Score 157;  DB 1;  Length 58;
  Best Local Similarity   70.2%;  Pred. No. 1.5e-13;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              ||||||||||||||||||||||||||||||   |  : | :|  | |::
Db          6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 50


RESULT 4
A4_SHEEP
ID   A4_SHEEP       STANDARD;      PRT;    58 AA.
AC   Q28757;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
```

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RC   TISSUE=Heart;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56130; CAA39595.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   DOMAIN       58    >58       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6300 MW;  F434209D88EBA82D CRC64;

  Query Match             63.6%;  Score 157;  DB 1;  Length 58;
  Best Local Similarity   70.2%;  Pred. No. 1.5e-13;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||||||||||||||||||||||||||||   |  : | :|  | |::
Db          6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 50


RESULT 5
A4_BOVIN
ID   A4_BOVIN       STANDARD;      PRT;    59 AA.
AC   Q28053;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56124; CAA39589.1; -.
DR   EMBL; X56126; CAA39591.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     58       POTENTIAL.
FT   DOMAIN       59    >59       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      59     59
SQ   SEQUENCE   59 AA;  6414 MW;  F43469D488A2E12D CRC64;

  Query Match             63.6%;  Score 157;  DB 1;  Length 59;
  Best Local Similarity   70.2%;  Pred. No. 1.5e-13;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||||||||||||||||||||||||||||   |  : | :|  | |::
Db          7 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 51


RESULT 6
A4_SAISC
ID   A4_SAISC       STANDARD;      PRT;    751 AA.
AC   Q95241;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
DE   APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
DE   Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
DE   CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Liver;
RX   MEDLINE=96108492; PubMed=8532114;
RA   Levy E., Amorim A., Frangione B., Walker L.C.;
RT   "Beta-amyloid precursor protein gene in squirrel monkeys with
RT   cerebral amyloid angiopathy.";
RL   Neurobiol. Aging 16:805-808(1995).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(0) alpha ATPase activity (By similarity).
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```
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=Q95241-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q95241-2; Sequence=Not described;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; S81024; AAD14347.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Amyloid; Alternative splicing.
FT   SIGNAL       1    17       BY SIMILARITY.
FT   CHAIN       18   751       A4 PROTEIN.
FT   CHAIN       18   668       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN       18   652       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN      653   751       C99 (POTENTIAL).
FT   CHAIN      653   694       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN      653   692       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN      669   751       C83 (POTENTIAL).
FT   CHAIN      669   694       P3(42) (POTENTIAL).
FT   CHAIN      669   692       P3(40) (POTENTIAL).
FT   CHAIN      693   751       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN      695   751       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN      702   751       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN      721   751       C31 (POTENTIAL).
FT   DOMAIN      18   680       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   681   704       POTENTIAL.
FT   DOMAIN     705   751       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      96   110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     181   188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN     291   341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN     316   344       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     363   428       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     504   521       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN     713   732       INTERACTION WITH G(O)-ALPHA
FT                              (BY SIMILARITY).
FT   DOMAIN     230   260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN     274   280       POLY-THR.
FT   SITE       144   144       REQUIRED FOR COPPER(II) REDUCTION
FT                              (BY SIMILARITY).
FT   ACT_SITE   301   302       REACTIVE BOND.
FT   SITE       652   653       CLEAVAGE (BY BETA-SECRETASE)
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FT                                   (BY SIMILARITY).
FT   SITE        653    654          CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        668    669          CLEAVAGE (BY ALPHA-SECRETASE)
FT                                   (BY SIMILARITY).
FT   SITE        685    685          INVOLVED IN FREE RADICAL PROPAGATION
FT                                   (BY SIMILARITY).
FT   SITE        687    687          INVOLVED IN OXIDATIVE REACTIONS
FT                                   (BY SIMILARITY).
FT   SITE        692    693          CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                   (BY SIMILARITY).
FT   SITE        694    695          CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                   (BY SIMILARITY).
FT   SITE        701    702          CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                   (BY SIMILARITY).
FT   SITE        705    715          BASOLATERAL SORTING SIGNAL
FT                                   (BY SIMILARITY).
FT   SITE        720    721          CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT                                   (BY SIMILARITY).
FT   SITE        738    741          ENDOCYTOSIS SIGNAL.
FT   SITE        740    743          NPXY MOTIF.

  Query Match           63.6%;  Score 157;  DB 1;  Length 751;
  Best Local Similarity  70.2%;  Pred. No. 2e-12;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||||||||||||||||||||||||||||    |  : | :|  | |::
Db        653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 697


RESULT 7
A4_CAVPO
ID   A4_CAVPO       STANDARD;      PRT;   770 AA.
AC   Q60495; Q60496;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
DE   protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
DE   P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE   CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
GN   APP.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Liver;
RX   MEDLINE=97236426; PubMed=9116031;
RA   Beck M., Mueller D., Bigl V.;
RT   "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT   alternative splicing.";
RL   Biochim. Biophys. Acta 1351:17-21(1997).
RN   [2]
RP   INTERACTION OF BETA-APP40 WITH APOE.
RX   MEDLINE=98007700; PubMed=9349544;
RA   Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
RA   Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
RT   "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
RT   cerebral capillary sequestration and blood-brain barrier transport of
RT   circulating Alzheimer's amyloid beta.";
RL   J. Neurochem. 69:1995-2004(1997).
RN   [3]
RP   PROCESSING.
RX   MEDLINE=20084499; PubMed=10619481;
RA   Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA   Bigl V.;
RT   "Guinea-pig primary cell cultures provide a model to study expression
RT   and amyloidogenic processing of endogenous amyloid precursor
RT   protein.";
RL   Neuroscience 95:243-254(2000).
RN   [4]
RP   GAMMA-SECRETASE PROCESSING.
RX   MEDLINE=20576391; PubMed=11035007;
RA   Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA   Ziani-Cherif C., Onstead L., Sambamurti K.;
RT   "A novel gamma -secretase assay based on detection of the putative
RT   C-terminal fragment-gamma of amyloid beta protein precursor.";
RL   J. Biol. Chem. 276:481-487(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC       and apoliproteins E and J in the CSF and to HDL particles in
CC       plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) and DDB1 (By similarity).
CC       Associates with microtubules in the presence of ATP and in a
CC       kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC       all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC       ApoE3 appears to be the preferred amyloid binding isoform, while
CC       the apoE4 isoform-beta-APP40 complex is capable of being
CC       transported across the blood-brain barrier.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated pits
CC       (By similarity). During maturation, the immature APP (N-
CC       glycosylated in the endoplasmic reticulum) moves to the Golgi
CC       complex where complete maturation occurs (O-glycosylated and
CC       sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC       APP is released into the extracellular space and the C-terminal is
CC       internalized to endosomes and lysosomes (By similarity). Some APP
CC       accumulates in secretory transport vesicles leaving the late Golgi
CC       compartment and returns to the cell surface (By similarity). APP
CC       sorts to the basolateral surface in epithelial cells (By
CC       similatity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms, missing exons 7,8 and 15, seem to
CC         exist. The L-isoforms, missing exon 15, are referred to as
CC         appicans;
CC       Name=APP770;
CC         IsoId=Q60495-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
CC   -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC       brain. The longer isoforms containing the BPTI domain are
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CC       predominantly expressed in peripheral organs such as muscle and
CC       liver.
CC   -!- INDUCTION: Increased levels during neuronal differentiation.
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells.
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue (By similarity). The NPXY site is also involved in
CC       clathrin-mediated endocytosis.
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC       gamma-secretase yields P3 peptides. This is the major secretory
CC       pathway and is nonamyloidogenic. Alternatively,
CC       presenilin/nicastrin-mediated gamma-secretase processing of CTF-
CC       beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC       and amyloid-beta 42 (Abeta42), major components of amyloid
CC       plaques, and the corresponding cytotoxic C-terminal fragments
CC       (CTFs).
CC   -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC       apoptosis (By similarity).
CC   -!- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
CC       the L-APP isoforms produces the APP proteoglycan core proteins,
CC       the appicans (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific (By similarity).
CC       Phosphorylation can affect APP processing, neuronal
CC       differentiation and interaction with other proteins.
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X97631; CAA66230.1; -.
DR   EMBL; X99198; CAA67589.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1    17       BY SIMILARITY.
FT   CHAIN        18   770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18   687       SOLUBLE APP-ALPHA (BY SIMILARITY).
FT   CHAIN        18   671       SOLUBLE APP-BETA (BY SIMILARITY).
FT   CHAIN       672   770       CTF-ALPHA (BY SIMILARITY).
FT   CHAIN       672   713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672   711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688   770       CTF-BETA (BY SIMILARITY).
FT   CHAIN       688   713       P3(42) (BY SIMILARITY).
FT   CHAIN       688   711       P3(40) (BY SIMILARITY).
FT   CHAIN       712   770       GAMMA-CTF(59) (BY SIMILARITY).
FT   CHAIN       714   770       GAMMA-CTF(57) (BY SIMILARITY).

  Query Match          63.6%;  Score 157;  DB 1;  Length 770;
  Best Local Similarity  70.2%;  Pred. No. 2.1e-12;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||||||||||||||||||||||||||||||||||    | : | :|  | |::
Db        672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 716


RESULT 8
A4_HUMAN
ID   A4_HUMAN        STANDARD;      PRT;   770 AA.
AC   P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
AC   Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCC8; Q9UCD1; Q9UQ58;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE   nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE   alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE   (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE   P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE   (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE   secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE   (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE   (Amyloid intracellular domain 50) (AID(50)); C31].
GN   APP OR A4 OR AD1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=87144572; PubMed=2881207;
RA   Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA   Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT   "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT   cell-surface receptor.";
RL   Nature 325:733-736(1987).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM APP751).
RC   TISSUE=Brain;
RX   MEDLINE=88122639; PubMed=2893289;
RA   Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA   Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA   Cordell B.;
RT   "A new A4 amyloid mRNA contains a domain homologous to serine
RT   proteinase inhibitors.";
RL   Nature 331:525-527(1988).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RX   MEDLINE=89128427; PubMed=2783775;
RA   Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA   Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT   "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT   is encoded by 16 exons.";
RL   Nucleic Acids Res. 17:517-522(1989).
```

RN [4]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";
RL Gene 87:257-263(1990).
RN [5]
RP ERRATUM, AND REVISIONS.
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RL Gene 102:291-292(1991).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
RC TISSUE=Leukocyte;
RX MEDLINE=92268136; PubMed=1587857;
RA Koenig G., Moenning U., Czech C., Prior R., Banati R.,
RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
RT "Identification and differential expression of a novel alternative
RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
RT leukocytes and brain microglial cells.";
RL J. Biol. Chem. 267:10804-10809(1992).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM APP639).
RC TISSUE=Brain;
RX MEDLINE=22744650; PubMed=12859342;
RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
RT "Identification of a novel alternative splicing isoform of human
RT amyloid precursor protein gene, APP639.";
RL Eur. J. Neurosci. 18:102-108(2003).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM APP305).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [11]
RP ERRATUM, AND REVISIONS.
RA Mita S., Sadlock J., Herbert J., Schon E.A.;
RL Nucleic Acids Res. 16:11402-11402(1988).
RN [12]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE=89165870; PubMed=2538123;
RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
RT "Characterization of the 5'-end region and the first two exons of the
RT beta-protein precursor gene.";
RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
RN [13]
RP SEQUENCE OF 18-50.
RC TISSUE=Fibroblast;
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [14]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=89346754; PubMed=2569763;
RA de Sauvage F., Octave J.N.;
RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT secreted protein.";
RL Science 245:651-653(1989).
RN [15]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [16]
RP SEQUENCE OF 286-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [17]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [18]
RP SEQUENCE OF 507-770 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [19]
RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX MEDLINE=96139497; PubMed=8576160;
RA Beher D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [20]
RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717
RP AND AD GLY-717.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzcwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
RN [21]
RP SEQUENCE OF 656-737 FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;

```
RA   Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA   Little S.P.;
RT   "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT   similarity to soybean trypsin inhibitor.";
RL   Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN   [22]

  Query Match             63.6%;  Score 157;  DB 1;  Length 770;
  Best Local Similarity   70.2%;  Pred. No. 2.1e-12;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||||||||||||||||||||||||||||   |  : | :|  | |::
Db        672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 716


RESULT 9
A4_MACFA
ID   A4_MACFA       STANDARD;      PRT;   770 AA.
AC   P53601; Q95KN7;
DT   01-OCT-1996 (Rel. 34, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC   TISSUE=Cerebellum;
RX   MEDLINE=91273117; PubMed=1905108;
RA   Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT   "Homology of the amyloid beta protein precursor in monkey and human
RT   supports a primate model for beta amyloidosis in Alzheimer's
RT   disease.";
RL   Am. J. Pathol. 138:1423-1435(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=P53601-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
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CC   ----------------------------------------------------------------------
DR   EMBL; M58727; AAA36829.1; -.
DR   EMBL; M58726; AAA36828.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672    770       C99 (POTENTIAL).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN       688    770       C83 (POTENTIAL).
FT   CHAIN       688    713       P3(42) (POTENTIAL).
FT   CHAIN       688    711       P3(40) (POTENTIAL).
FT   CHAIN       712    770       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN       714    770       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN       721    770       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN       740    770       C31 (POTENTIAL).
FT   DOMAIN       18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    700    723       POTENTIAL.
FT   DOMAIN      724    770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      391    423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      491    522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      523    540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      732    751       INTERACTION WITH G(O)-ALPHA
FT                                (BY SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND (BY SIMILARITY).
FT   SITE        671    672       CLEAVAGE (BY BETA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        672    673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        687    688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        704    704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                                (BY SIMILARITY).
FT   SITE        706    706       INVOLVED IN OXIDATIVE REACTIONS
FT                                (BY SIMILARITY).
FT   SITE        711    712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                (BY SIMILARITY).
FT   SITE        713    714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                (BY SIMILARITY).
FT   SITE        720    721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                (BY SIMILARITY).
FT   SITE        724    734       BASOLATERAL SORTING SIGNAL
FT                                (BY SIMILARITY).
FT   SITE        739    740       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
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  Query Match           63.6%;  Score 157;  DB 1;  Length 770;
  Best Local Similarity   70.2%;  Pred. No. 2.1e-12;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGIISITEIKGVIVHRIETIL 47
              |||||||||||||||||||||||||||||   |  : | :|  | |::
Db        672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 716


RESULT 10
A4_PIG
ID   A4_PIG          STANDARD;      PRT;   770 AA.
AC   P79307; Q29023; Q9TUI0;
DT   01-NOV-1997 (Rel. 35, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura A., Takahashi T.;
RT   "Amyloid precursor protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-136 FROM N.A.
RC   TISSUE=Small intestine;
RA   Winteroe A.K., Fredholm M.;
RT   "Evaluation and characterization of a porcine small intestine cDNA
RT   library.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 667-723 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
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CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB032550; BAA84580.1; -.
DR   EMBL; Z84022; CAB06313.1; -.
DR   EMBL; X56127; CAA39592.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Amyloid.
FT   SIGNAL        1    17       BY SIMILARITY.
FT   CHAIN        18   770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18   687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18   671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672   770       C99 (BY SIMILARITY).
FT   CHAIN       672   713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672   711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688   770       C83 (BY SIMILARITY).
FT   CHAIN       688   713       P3(42) (BY SIMILARITY).
FT   CHAIN       688   711       P3(40) (BY SIMILARITY).
FT   CHAIN       712   770       GAMMA-CTF(59).
FT   CHAIN       714   770       GAMMA-CTF(57).
FT   CHAIN       721   770       GAMMA-CTF(50) (BY SIMILARITY).
FT   CHAIN       740   770       C31 (DURING APOPTOSIS) (BY SIMILARITY).
FT   DOMAIN       18   699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    700   723       POTENTIAL.
FT   DOMAIN      724   770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96   110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      135   155       COPPER-BINDING (BY SIMILARITY).
FT   DOMAIN      181   188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291   341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      391   423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      491   522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      523   540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      732   751       INTERACTION WITH G(O)-ALPHA (BY
FT                               SIMILARITY).
FT   DOMAIN      230   260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274   280       POLY-THR.
FT   SITE        144   144       REQUIRED FOR COPPER(II) REDUCTION
FT                               (BY SIMILARITY).
FT   ACT_SITE    301   302       REACTIVE BOND (BY SIMILARITY).
FT   SITE        671   672       CLEAVAGE (BY BETA-SECRETASE)
FT                               (BY SIMILARITY).
FT   SITE        672   673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        687   688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                               (BY SIMILARITY).
FT   SITE        704   704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                               (BY SIMILARITY).
FT   SITE        706   706       INVOLVED IN OXIDATIVE REACTIONS
FT                               (BY SIMILARITY).
FT   SITE        711   712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                               (BY SIMILARITY).
FT   SITE        713   714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                               (BY SIMILARITY).
FT   SITE        720   721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)

  Query Match           63.6%;  Score 157;  DB 1;  Length 770;
  Best Local Similarity 70.2%;  Pred. No. 2.1e-12;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||||||||||||||||||||||||||||||   | : | :|  | |::
Db        672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 716
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RESULT 11
A4_MOUSE
ID   A4_MOUSE       STANDARD;      PRT;   770 AA.
AC   P12023; P97487; P97942; Q99K32;
DT   01-OCT-1989 (Rel. 12, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:
DE   Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
DE   (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
DE   40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
DE   C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE   (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
DE   (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
DE   (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
DE   50) (AID(50)); C31].
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88106489; PubMed=3322280;
RA   Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT   "Complementary DNA for the mouse homolog of the human amyloid beta
RT   protein precursor.";
RL   Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN   [2]
RP   REVISIONS.
RA   Yamada T.;
RL   Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=BALB/c; TISSUE=Brain;
RX   MEDLINE=92096458; PubMed=1756177;
RA   de Strooper B., van Leuven F., van den Berghe H.;
RT   "The amyloid beta protein precursor or proteinase nexin II from mouse
RT   is closer related to its human homolog than previously reported.";
RL   Biochim. Biophys. Acta 1129:141-143(1991).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=SAMP8; TISSUE=Hippocampus;
RX   MEDLINE=21130647; PubMed=11235921;
RA   Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
RA   Alvarez J., Morley J.E.;
RT   "Molecular cloning, expression, and regulation of hippocampal amyloid
RT   precursor protein of senescence accelerated mouse (SAMP8).";
RL   Biochem. Cell Biol. 79:57-67(2001).
RN   [5]
RP   SEQUENCE OF 1-19 FROM N.A.
RX   MEDLINE=92209998; PubMed=1555768;
RA   Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA   Sakai Y.;
RT   "Positive and negative regulatory elements for the expression of the
RT   Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL   Gene 112:189-195(1992).
RN   [6]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
RC   TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [7]
RP   SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Kidney;
RX   MEDLINE=89149813; PubMed=2493250;
RA   Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
RT   "Structure and expression of the alternatively-spliced forms of mRNA
RT   for the mouse homolog of Alzheimer's disease amyloid beta protein
RT   precursor.";
RL   Biochem. Biophys. Res. Commun. 158:906-912(1989).
RN   [8]
RP   SEQUENCE OF 289-364 FROM N.A.
RC   STRAIN=CD-1; TISSUE=Placenta;
RX   MEDLINE=89345111; PubMed=2569710;
RA   Fukuchi K., Martin G.M., Deeb S.S.;
RT   "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT   precursor of Mus domesticus.";
RL   Nucleic Acids Res. 17:5396-5396(1989).
RN   [9]
RP   SEQUENCE OF 656-737 FROM N.A.
RC   STRAIN=129/Sv;
RA   Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
RA   Loring J.F., Goate A.M.;
RT   "Introduction of six mutations into the mouse genome using 'Hit and
RT   Run' gene-targeting: introduction of familial Alzheimer's disease
RT   mutations into the mouse amyloid precursor protein gene and
RT   humanization of the A-beta fragment.";
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN   [10]
RP   TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
RX   MEDLINE=93287808; PubMed=8510506;
RA   Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
RT   "Regional distribution of the alternatively spliced isoforms of beta
RT   APP RNA transcript in the brain of normal, heterozygous and
RT   homozygous weaver mutant mice as revealed by in situ hybridization
RT   histochemistry.";
RL   Brain Res. Mol. Brain Res. 17:340-346(1993).
RN   [11]
RP   INTERACTION WITH KNS2.
RX   MEDLINE=21010507; PubMed=11144355;
RA   Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
RT   "Axonal transport of amyloid precursor protein is mediated by direct
RT   binding to the kinesin light chain subunit of kinesin-I.";
RL   Neuron 28:449-459(2000).
RN   [12]
RP   C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
RP   THR-743; TYR-757; ASN-759 AND TYR-762.
RX   MEDLINE=21408156; PubMed=11517249;
RA   Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA   Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
RA   Kyriakis J.M., Nishimoto I.;
RT   "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
RT   scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL   J. Neurosci. 21:6597-6607(2001).
RN   [13]
RP   INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
RX   MEDLINE=22028091; PubMed=11912189;
RA   Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
RT   "Interaction of Alzheimer's beta-amyloid precursor family proteins
RT   with scaffold proteins of the JNK signaling cascade.";
RL   J. Biol. Chem. 277:20070-20078(2002).
RN   [14]
```

```
RP   INTERACTION OF CTF PEPTIDES WITH NUMB.
RX   MEDLINE=22008109; PubMed=12011466;
RA   Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
RA   Meucci O., McGlade J.C., Rakic P., D'Adamio L.;
RT   "The gamma-secretase-generated intracellular domain of beta-amyloid
RT   precursor protein binds Numb and inhibits Notch signaling.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
RN   [15]
RP   GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.
RX   MEDLINE=21437805; PubMed=11553691;
RA   Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
RT   "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
RT   gamma-secretase is rapidly degraded but distributes partially in a
RT   nuclear fraction of neurones in culture.";
RL   J. Neurochem. 78:1168-1178(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions. Can promote transcription activation through binding
CC       to APBB1/Tip60 and inhibit Notch signaling through interaction
CC       with Numb. Couples to apoptosis-inducing pathways such as those
CC       mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity (By
CC       similarity). Acts as a kinesin I membrane receptor, mediating the
CC       axonal transport of beta-secretase and presenilin 1. May be
CC       involved in copper homeostasis/oxidative stress through copper ion
CC       reduction. Can regulate neurite outgrowth through binding to
CC       components of the extracellular matrix such as heparin and
CC       collagen I and IV (By similarity). The splice isoforms that
CC       contain the BPTI domain possess protease inhibitor activity (By
CC       similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC       only weakly transient metals and have little reducing activity due
CC       to substitutions of transient metal chelating residues. Beta-APP42
CC       may activate mononuclear phagocytes in the brain and elicit
CC       inflammatory responses. Promotes both tau aggregation and TPK II-
CC       mediated phosphorylation (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis.
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
CC       its serine phosphorylation. Also interacts with GPCR-like protein
CC       BPP, FPRL1, APPBP1, IB1, KNS2 (via its TPR domains), APPBP2 (via
CC       BaSS) and DDB1 (By similarity). In vitro, it binds MAPT via the
CC       MT-binding domains (By similarity). Associates with microtubules
CC       in the presence of ATP and in a kinesin-dependent manner (By
CC       similarity). Interacts, through a C-terminal domain, with GNAO1
CC       (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
CC       neurons (By similarity). Beta-amyloid associates with HADH2 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete

  Query Match             55.9%;  Score 138;  DB 1;  Length 770;
  Best Local Similarity   63.8%;  Pred. No. 5.8e-10;
  Matches   30;  Conservative    5;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||| ||||:|| ||||||||||||||    | : | :|  | |::
Db        672 DAEFGHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 716


RESULT 12
A4_RAT
ID   A4_RAT          STANDARD;      PRT;   770 AA.
AC   P08592;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble
DE   APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
DE   amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
DE   C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
DE   fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
DE   Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
GN   APP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88312583; PubMed=2900758;
RA   Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA   Seeburg P.H.;
RT   "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT   in rat brain suggests a role in cell contact.";
RL   EMBO J. 7:1365-1370(1988).
RN   [2]
RP   SEQUENCE OF 289-364 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=89183625; PubMed=2648331;
RA   Kang J., Mueller-Hill B.;
RT   "The sequence of the two extra exons in rat preA4.";
RL   Nucleic Acids Res. 17:2130-2130(1989).
RN   [3]
RP   SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
RX   MEDLINE=21443797; PubMed=11483588;
RA   Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
RT   "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT   family resembling gamma-secretase-like cleavage of Notch.";
RL   J. Biol. Chem. 276:35235-35238(2001).
RN   [4]
RP   ALTERNATIVE SPLICING.
RX   MEDLINE=96187032; PubMed=8624099;
RA   Sandbrink R., Masters C.L., Beyreuther K.;
RT   "APP gene family. Alternative splicing generates functionally related
RT   isoforms.";
RL   Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN   [5]
RP   TISSUE SPECIFICITY OF APPICAN.
RX   MEDLINE=95263526; PubMed=7744833;
RA   Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,
RA   Mytilineou C., Margolis R.U., Robakis N.K.;
RT   "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT   brain and is produced by astrocytes but not by neurons in primary
RT   neural cultures.";
RL   J. Biol. Chem. 270:11839-11844(1995).
RN   [6]
RP   TISSUE SPECIFICITY OF ISOFORMS.
RX   MEDLINE=97150061; PubMed=8996834;
RA   Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
RT   "Expression of the APP gene family in brain cells, brain development
RT   and aging.";
RL   Gerontology 43:119-131(1997).
RN   [7]
RP   INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
RP   TYR-762.
RX   MEDLINE=99127916; PubMed=9930726;
RA   Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
RA   Suzuki T., Nairn A.C., Greengard P.;
RT   "A 127-kDa protein (UV-DDB) binds to the cytoplasmic domain of the
RT   Alzheimer's amyloid precursor protein.";
RL   J. Neurochem. 72:549-556(1999).
RN   [8]
RP   INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.
RX   MEDLINE=99162676; PubMed=10024358;
RA   Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouillot C.,
```

RA Valenza C., Prochiantz A., Allinquant B.;
RT "The amyloid precursor protein interacts with Go heterotrimeric
RT protein within a cell compartment specialized in signal
RT transduction.";
RL J. Neurosci. 19:1717-1727(1999).
RN [9]
RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
RX MEDLINE=95256193; PubMed=7737970;
RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
RT "The chondroitin sulfate attachment site of appican is formed by
RT splicing out exon 15 of the amyloid precursor gene.";
RL J. Biol. Chem. 270:10388-10391(1995).
RN [10]
RP BETA-AMYLOID METAL-BINDING.
RX MEDLINE=99316162; PubMed=10386999;
RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
RA Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
RA Bush A.I.;
RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
RT peroxide through metal ion reduction.";
RL Biochemistry 38:7609-7616(1999).
RN [11]
RP BETA-AMYLOID ZINC BINDING.
RX MEDLINE=99343552; PubMed=10413512;
RA Liu S.T., Howlett G., Barrow C.J.;
RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
RT of the A beta peptide of Alzheimer's disease.";
RL Biochemistry 38:9373-9378(1999).
RN [12]
RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
RP GLY-704.
RX MEDLINE=21956095; PubMed=11959460;
RA Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;
RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
RT peptide 1-42-associated oxidative stress and neurotoxicity.";
RL Biochim. Biophys. Acta 1586:190-198(2001).
RN [13]
RP PHOSPHORYLATION.
RX MEDLINE=97239592; PubMed=9085254;
RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
RA Greengard P., Suzuki T.;
RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
RT phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
RT cultured cells.";
RL Mol. Med. 3:111-123(1997).
RN [14]
RP PHOSPHORYLATION ON SER-730.
RX MEDLINE=99262094; PubMed=10329382;
RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
RA Greengard P., Nairn A.C., Suzuki T.;
RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
RT precursor protein at Ser655 by a novel protein kinase.";
RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
RN [15]
RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
RP THR-743.
RX MEDLINE=99274744; PubMed=10341243;
RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
RA Kirino Y., Greengard P., Suzuki T.;
RT "Role of phosphorylation of Alzheimer's amyloid precursor protein
RT during neuronal differentiation.";
RL J. Neurosci. 19:4421-4427(1999).
RN [16]
RP PHOSPHORYLATION ON THR-743.
RX MEDLINE=20396183; PubMed=10936190;
RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
RT protein by cyclin-dependent kinase 5.";
RL J. Neurochem. 75:1085-1091(2000).
RN [17]
RP CARBOHYDRATE STRUCTURE OF APPICAN.
RX MEDLINE=21463085; PubMed=11479316;
RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
RA Sugahara K., Robakis N.K.;
RT "Appican, the proteoglycan form of the amyloid precursor protein,
RT contains chondroitin sulfate E in the repeating disaccharide region
RT and 4-O-sulfated galactose in the linkage region.";
RL J. Biol. Chem. 276:37155-37160(2001).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP. Inhibits
CC G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
CC mediating the axonal transport of beta-secretase and presenilin 1
CC (By similarity). May be involved in copper homeostasis/oxidative
CC stress through copper ion reduction. Can regulate neurite
CC outgrowth through binding to components of the extracellular
CC matrix such as heparin and collagen I and IV (By similarity). The
CC splice isoforms that contain the BPTI domain possess protease
CC inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC only weakly transient metals and have little reducing activity due
CC to substitutions of transient metal chelating residues. Beta-APP42
CC may activate mononuclear phagocytes in the brain and elicit
CC inflammatory responses. Promotes both tau aggregation and TPK II-
CC mediated phosphorylation (By similarity).
CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC extracellular matrix and may regulate neurite outgrowth in the
CC brain.
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC (via its TPR domains), APPBP2 (via BaSS) (By similarity) and DDB1.
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity). Interacts,
CC through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
CC CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
CC associates with HADH2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the

Query Match 55.9%; Score 138; DB 1; Length 770;
Best Local Similarity 63.8%; Pred. No. 5.8e-10;
Matches 30; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
Db 672 DAEFGHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 716

RESULT 13
A4_TETFL
ID A4_TETFL STANDARD; PRT; 780 AA.
AC O73683;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE Beta-amyloid protein (Beta-APP) (A-beta)].
GN APP.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=47145;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98252138; PubMed=9599080;
RA   Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT   "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL   Gene 210:17-24(1998).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF018165; AAC41275.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Serine protease inhibitor.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    780       ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT                                HOMOLOG.
FT   CHAIN       682    724       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       19    711       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    712    732       POTENTIAL.
FT   DOMAIN      733    780       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      323    382       BPTI/KUNITZ INHIBITOR.
FT   SITE        769    772       CLATHRIN-BINDING (BY SIMILARITY).
FT   DISULFID    327    378       BY SIMILARITY.
FT   DISULFID    336    361       BY SIMILARITY.
FT   CARBOHYD    560    560       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   780 AA;  88238 MW;  60071BE945201910 CRC64;

  Query Match             46.6%;  Score 115;  DB 1;  Length 780;
  Best Local Similarity   55.3%;  Pred. No. 5.3e-07;
  Matches   26;  Conservative    6;  Mismatches   13;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              : | |  : ||||||||||||||||||    |  : | :|  | ||::
Db        682 ETEDRQSTEYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 726


RESULT 14
A4_FUGRU
ID   A4_FUGRU       STANDARD;      PRT;   737 AA.
AC   O93279;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE   Beta-amyloid protein (Beta-APP) (A-beta)].
GN   APP.
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98252138; PubMed=9599080;
RA   Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT   "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL   Gene 210:17-24(1998).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF090120; AAD13392.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; FALSE_NEG.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Serine protease inhibitor.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    737       ALZHEIMER'S DISEASE AMYLOID A4
FT                                PROTEIN HOMOLOG.
FT   CHAIN       639    681       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       19    668       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    669    689       POTENTIAL.
FT   DOMAIN      690    737       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      286    344       BPTI/KUNITZ INHIBITOR.
FT   SITE        726    729       CLATHRIN-BINDING (BY SIMILARITY).
FT   ACT_SITE    300    301       REACTIVE BOND.
FT   DISULFID    290    340       BY SIMILARITY.
FT   DISULFID    299    323       BY SIMILARITY.
FT   DISULFID    315    336       BY SIMILARITY.
FT   CARBOHYD    522    522       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   737 AA;  82856 MW;  6FAD01E2E3B2B7E2 CRC64;

  Query Match             44.9%;  Score 111;  DB 1;  Length 737;
  Best Local Similarity   51.1%;  Pred. No. 1.6e-06;
  Matches   24;  Conservative    9;  Mismatches   12;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
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              : : |  :||||:||||||||:||||||   |  : | :|  | |::
Db        639 ETDKRQSAGYEVYHQKLVFFADDVGSNKGAIIGLMVGGVV--IATVI 683


RESULT 15
VGLF_RINDL
ID   VGLF_RINDL     STANDARD;      PRT;   546 AA.
AC   P10864;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   F.
OS   Rinderpest virus (strain L) (RDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11243;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88219541; PubMed=3285575;
RA   Tsukiyama K., Yoshikawa Y., Yamanouchi K.;
RT   "Fusion glycoprotein (F) of rinderpest virus: entire nucleotide
RT   sequence of the F mRNA, and several features of the F protein.";
RL   Virology 164:523-530(1988).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC       LINKED BY A DISULFIDE BOND.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M20870; AAA47399.1; -.
DR   PIR; A28921; VGNZRL.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; fusion_gly; 1.
KW   Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    546       FUSION GLYCOPROTEIN F0.
FT   CHAIN       20    108       F2 PROTEIN.
FT   CHAIN      109    546       F1 PROTEIN.
FT   DOMAIN     104    108       ARG/LYS-RICH (BASIC).
FT   TRANSMEM   109    133       POTENTIAL.
FT   TRANSMEM   484    513       POTENTIAL.
FT   DOMAIN     514    517       ARG/LYS-RICH (BASIC).
FT   DISULFID    64    191       LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT   CARBOHYD    25     25       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    57     57       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    63     63       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   546 AA;  58911 MW;  985029418F28FPB5 CRC64;

  Query Match             25.9%;  Score 64;  DB 1;  Length 546;
  Best Local Similarity   61.1%;  Pred. No. 1.3;
  Matches   11;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         31 SITEIKGVIVHRIETILP 48
              |::|||||||||:|:: :
Db        283 SLSEIKGVIVHRLESVSY 300


Search completed: June 18, 2004, 19:59:39
Job time : 10.4233 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:53:15 ; Search time 46.5276 Seconds
(without alignments)
325.503 Million cell updates/sec

Title: US-09-865-294A-74
Perfect score: 247
Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....KISITEIKGVIVHRIETILF 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	163	66.0	82	4	Q16014	Q16014 homo sapien
2	157	63.6	82	4	Q16020	Q16020 homo sapien
3	157	63.6	82	4	Q16019	Q16019 homo sapien
4	157	63.6	113	13	Q8JH58	Q8jh58 chelydra se
5	157	63.6	534	13	O93296	O93296 gallus gall
6	157	63.6	695	13	Q9DGJ8	Q9dgj8 gallus gall
7	157	63.6	751	13	Q9DGJ7	Q9dgj7 gallus gall
8	156.5	63.4	569	13	Q9PVL1	Q9pvl1 gallus gall
9	152	61.5	30	4	Q9UCA9	Q9uca9 homo sapien
10	152	61.5	33	4	Q9UC33	Q9uc33 homo sapien
11	147	59.5	28	4	Q9UCD1	Q9ucd1 homo sapien
12	138	55.9	79	11	O35463	O35463 cricetulus
13	138	55.9	218	11	Q8BPV5	Q8bpv5 mus musculu
14	138	55.9	384	11	Q8BPC7	Q8bpc7 mus musculu
15	138	55.9	693	13	Q98SG0	Q98sg0 xenopus lae
16	138	55.9	747	13	Q91963	Q91963 xenopus. ap
17	135	54.7	695	13	Q98SP9	Q98sf9 xenopus lae
18	135	54.7	695	13	Q7ZXQ0	Q7zxq0 xenopus lae
19	128	51.8	699	13	O57394	O57394 narke japon
20	106	42.9	19	4	Q9UCC8	Q9ucc8 homo sapien
21	98.5	39.9	357	13	Q8UUI8	Q8uui8 brachydanio
22	98.5	39.9	472	13	Q8UUS0	Q8uus0 brachydanio
23	98.5	39.9	612	13	Q9I9E7	Q9i9e7 brachydanio
24	98.5	39.9	678	13	Q7ZZT1	Q7zzt1 brachydanio
25	98.5	39.9	738	13	Q90W28	Q90w28 brachydanio
26	96	38.9	239	13	Q8UUI7	Q8uui7 brachydanio
27	96	38.9	694	13	Q8UUR9	Q8uur9 brachydanio
28	95	38.5	35	4	Q8WZ99	Q8wz99 homo sapien
29	63.5	25.7	663	16	Q9CJI4	Q9cji4 lactococcus
30	62	25.1	365	12	Q9WG05	Q9wg05 potato viru
31	62	25.1	528	12	Q9YJW9	Q9yjw9 canine dist
32	62	25.1	662	12	Q9DXZ2	Q9dxz2 canine dist
33	62	25.1	662	12	Q9YKL7	Q9ykl7 canine dist
34	62	25.1	662	12	O89327	O89327 canine dist
35	61	24.7	49	6	O97917	O97917 bos taurus
36	61	24.7	546	12	Q91HA5	Q91ha5 rinderpest
37	60	24.3	508	8	Q8W7S3	Q8w7s3 ternstroemi
38	60	24.3	508	8	Q8WIW2	Q8wiw2 anneslea fr
39	60	24.3	546	12	Q84926	Q84926 peste-des-p
40	60	24.3	662	12	Q91KN3	Q91kn3 canine dist
41	60	24.3	3063	12	Q8JQ05	Q8jq05 potato viru
42	59	23.9	292	12	Q85276	Q85276 potato viru
43	59	23.9	332	12	Q9DQN5	Q9dqn5 potato viru
44	59	23.9	337	12	Q8JPW2	Q8jpw2 potato viru
45	59	23.9	530	12	Q8QV06	Q8qv06 canine dist

ALIGNMENTS

RESULT 1
Q16014
ID Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzcwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26263.2; -.
DR HSSP; P05067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 66.0%; Score 163; DB 4; Length 82;
Best Local Similarity 70.8%; Pred. No. 8.2e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

```
Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETILF 48
              |||||||||||||||||||||||||||||    |  : | :|  | |::|
Db         18 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVIF 63
```

RESULT 2
Q16020

```
ID   Q16020      PRELIMINARY;      PRT;    82 AA.
AC   Q16020;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
GN   BETA APP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S61383; AAB26265.2; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8882 MW;  F534AA5AE5D9230A CRC64;

  Query Match             63.6%;  Score 157;  DB 4;  Length 82;
  Best Local Similarity   70.2%;  Pred. No. 5.1e-13;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||||||||||||||||||||||||||||    |  : | :|  | |::
Db         18 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 62


RESULT 3
Q16019
ID   Q16019      PRELIMINARY;      PRT;    82 AA.
AC   Q16019;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
GN   BETA APP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S61380; AAB26264.2; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8938 MW;  F534AA50E579230A CRC64;

  Query Match             63.6%;  Score 157;  DB 4;  Length 82;
  Best Local Similarity   70.2%;  Pred. No. 5.1e-13;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||||||||||||||||||||||||||||    |  : | :|  | |::
Db         18 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 62


RESULT 4
Q8JH58
ID   Q8JH58      PRELIMINARY;      PRT;   113 AA.
AC   Q8JH58;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid beta protein (Fragment).
OS   Chelydra serpentina serpentina (common snapping turtle).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX   NCBI_TaxID=134619;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21876906; PubMed=11882478;
RA   Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT   "Octylphenol (OP) alters the expression of members of the amyloid
RT   protein family in the hypothalamus of the snapping turtle, Chelydra
RT   serpentina serpentina.";
RL   Environ. Health Perspect. 110:269-275(2002).
DR   EMBL; AF541917; AAN04908.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   113 AA;  12750 MW;  72515C930496E053 CRC64;

  Query Match             63.6%;  Score 157;  DB 13;  Length 113;
  Best Local Similarity   70.2%;  Pred. No. 7.3e-13;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||||||||||||||||||||||||||||    |  : | :|  | |::
Db         15 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 59


RESULT 5
O93296
ID   O93296      PRELIMINARY;      PRT;   534 AA.
AC   O93296;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid protein (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98337885; PubMed=9671674;
RA   Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA   Milligan C.E.;
RT   "Increased production of amyloid precursor protein provides a
RT   substrate for caspase-3 in dying motoneurons.";
RL   J. Neurosci. 18:5869-5880(1998).
DR   EMBL; AF042098; AAC25052.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
```

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SQ   SEQUENCE   534 AA;  60597 MW;  FB53ECC2E66D4C92 CRC64;

  Query Match             63.6%;  Score 157;  DB 13;  Length 534;
  Best Local Similarity   70.2%;  Pred. No. 4.2e-12;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||||||||||||||||||||||||||||    |  : | :|  | |::
Db        436 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 480


RESULT 6
Q9DGJ8
ID   Q9DGJ8      PRELIMINARY;      PRT;   695 AA.
AC   Q9DGJ8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid precursor protein 695 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289218; AAG00593.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
SQ   SEQUENCE   695 AA;  78565 MW;  F201ED02AEC86D95 CRC64;

  Query Match             63.6%;  Score 157;  DB 13;  Length 695;
  Best Local Similarity   70.2%;  Pred. No. 5.7e-12;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||||||||||||||||||||||||||||    |  : | :|  | |::
Db        597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 641


RESULT 7
Q9DGJ7
ID   Q9DGJ7      PRELIMINARY;      PRT;   751 AA.
AC   Q9DGJ7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid precursor protein 751 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289219; AAG00594.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   751 AA;  84705 MW;  E78E9413A8033D84 CRC64;

  Query Match             63.6%;  Score 157;  DB 13;  Length 751;
  Best Local Similarity   70.2%;  Pred. No. 6.2e-12;
  Matches   33;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||||||||||||||||||||||||||||    |  : | :|  | |::
Db        653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 697


RESULT 8
Q9PVL1
ID   Q9PVL1      PRELIMINARY;      PRT;   569 AA.
AC   Q9PVL1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid protein (Fragment).
GN   APP.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT   "What the evolution of the amyloid protein precursor supergene family
RT   tells us about its function.";
RL   Neurochem. Int. 0:0-0(2000).
DR   EMBL; AF030341; AAF12698.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER      1      1
SQ   SEQUENCE   569 AA;  64753 MW;  0AB8BB851863A19D CRC64;

  Query Match             63.4%;  Score 156.5;  DB 13;  Length 569;
  Best Local Similarity   68.1%;  Pred. No. 5.3e-12;
  Matches   32;  Conservative    4;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISI-TEIKGVIVHRIETI 46
              |||||||||||||||||||||||||||||    |   : ||::  :  |
Db        472 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIANVIVI 518
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RESULT 9
Q9UCA9
ID   Q9UCA9      PRELIMINARY;      PRT;    30 AA.
AC   Q9UCA9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94153015; PubMed=8109908;
RA   Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;
RT   "The amino acid sequence of neuritic plaque amyloid from a familial
RT   Alzheimer's disease patient.";
RL   Ann. Neurol. 35:245-246(1994).
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   30 AA;  3391 MW;  FF4167ABD081160A CRC64;

  Query Match             61.5%;  Score 152;  DB 4;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNK 28
              ||||||||||||||||||||||||||||
Db          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNK 28


RESULT 10
Q9UC33
ID   Q9UC33      PRELIMINARY;      PRT;    33 AA.
AC   Q9UC33;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=93024877; PubMed=1406936;
RA   Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA   Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT   "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT   biological fluids.";
RL   Nature 359:325-327(1992).
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   33 AA;  3674 MW;  B1DEFE2F4167ABD0 CRC64;

  Query Match             61.5%;  Score 152;  DB 4;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-13;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNK 28
              ||||||||||||||||||||||||||||
Db          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNK 28


RESULT 11
Q9UCD1
ID   Q9UCD1      PRELIMINARY;      PRT;    28 AA.
AC   Q9UCD1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94045685; PubMed=8229004;
RA   Vigo-Pelfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;
RT   "Characterization of beta-amyloid peptide from human cerebrospinal
RT   fluid.";
RL   J. Neurochem. 61:1965-1968(1993).
DR   HSSP; P05067; 1AMB.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   28 AA;  3244 MW;  DE7BD081160AFC81 CRC64;

  Query Match             59.5%;  Score 147;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-12;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSN 27
              |||||||||||||||||||||||||||
Db          1 DAEFRHDSGYEVHHQKLVFFAEDVGSN 27


RESULT 12
O35463
ID   O35463      PRELIMINARY;      PRT;    79 AA.
AC   O35463;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Alzheimer's amyloid beta protein (Fragment).
GN   BETA APP.
OS   Cricetulus griseus (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Cricetulus.
OX   NCBI_TaxID=10029;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sambamurti K., Pinnix I., Gandhi S.;
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF030413; AAB86608.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER       1      1
FT   NON_TER      79     79
SQ   SEQUENCE   79 AA;  8538 MW;  37F2C6C3BFF3F597 CRC64;

  Query Match             55.9%;  Score 138;  DB 11;  Length 79;
  Best Local Similarity   63.8%;  Pred. No. 1.6e-10;
  Matches   30;  Conservative    5;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||| ||||:|| |||||||||||||||    |  : | :|  | |::
Db         21 DAEFGHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 65


RESULT 13
Q8BPV5
ID   Q8BPV5      PRELIMINARY;      PRT;   218 AA.
AC   Q8BPV5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
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DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid beta (Fragment).
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK052448; BAC34997.1; -.
DR   MGD; MGI:88059; App.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   218 AA;  24118 MW;  95B55AFDAE1D0EF5 CRC64;

  Query Match             55.9%;  Score 138;  DB 11;  Length 218;
  Best Local Similarity   63.8%;  Pred. No. 5e-10;
  Matches   30;  Conservative    5;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||| ||||:|| ||||||||||||||    |  : | :|  | |::
Db        120 DAEFGHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 164


RESULT 14
Q8BPC7
ID   Q8BPC7      PRELIMINARY;      PRT;   384 AA.
AC   Q8BPC7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid beta (Fragment).
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK076506; BAC36369.1; -.
DR   MGD; MGI:88059; App.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   384 AA;  43990 MW;  A81B1AD8AE683173 CRC64;

  Query Match             55.9%;  Score 138;  DB 11;  Length 384;
  Best Local Similarity   63.8%;  Pred. No. 9.4e-10;
  Matches   30;  Conservative    5;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |||| ||||:|| ||||||||||||||    |  : | :|  | |::
Db        286 DAEFGHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVV--IATVI 330


RESULT 15
Q98SG0
ID   Q98SG0      PRELIMINARY;      PRT;   693 AA.
AC   Q98SG0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid precursor protein A.
GN   APP.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van den Hurk W.H.;
RL   Thesis (2001), Department of Biological Sciences,
RL   University of Nijmegen, Nijmegen, Netherlands.
DR   EMBL; AJ298150; CAC37193.1; -.
DR   HSSP; P05067; 1HZ3.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
KW   Signal.
FT   SIGNAL        1     18       POTENTIAL.
SQ   SEQUENCE   693 AA;  78568 MW;  CAF1DF655C1AB653 CRC64;

  Query Match             55.9%;  Score 138;  DB 13;  Length 693;
  Best Local Similarity   59.6%;  Pred. No. 1.8e-09;
  Matches   28;  Conservative    8;  Mismatches    9;  Indels    2;  Gaps    1;

Qy          1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKKISITEIKGVIVHRIETIL 47
              |:|:|||: ||||||||||||:|||||    |  : | :|  | |::
Db        595 DSEYRHDTAYEVHHQKLVFFAEEVGSNKGAIIGLMVGGVV--IATVI 639


Search completed: June 18, 2004, 20:02:30
Job time : 47.5276 secs
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